

Accession	Gene	Accession	Gene	Accession	Gene
1	344	100.0	344	21	AAB18994
2	344	100.0	344	21	AAB18804
3	344	100.0	344	21	AAB18804
4	344	100.0	344	21	AAB08925
5	344	100.0	344	21	AAB08317
6	344	100.0	344	21	AAB08341
7	344	100.0	344	21	AAY93341
8	344	100.0	344	22	AA663598
9	344	100.0	344	22	AA667770
10	344	100.0	344	23	AA483995
	344	100.0	344	23	AA487796

84	9	2.6	1061	21	AA980568	Wild type Escheric	157	8	2.3	537	20	AA903839	Chimeric transcrip	
85	9	2.6	2639	22	ABG15016	Novel human diagno	158	8	2.3	550	14	AA42085	NF-kappaB p65.pro	
86	8	2.3	10	23	AB78543	Glycomodule relate	159	8	2.3	550	14	AA42254	Human p65 protein	
87	8	2.3	15	12	AA12480	"Hydrophobic tail"	160	8	2.3	550	14	AA42255	Human p65 protein	
88	8	2.3	26	20	AA03840	Alanine/proline ri	161	8	2.3	551	21	AA94383	Human NF-kappa-B p	
89	8	2.3	41	20	AA49097	Amino acid sequenc	162	8	2.3	581	22	AB59842	Drosophila melanog	
90	8	2.3	43	20	AA49096	Amino acid sequenc	163	8	2.3	609	19	AA83215	Human h-NUMB-R. H	
91	8	2.3	51	22	AAU62252	Protonibacterium	164	8	2.3	627	20	AA01495	Rat pan-s/tk recep	
92	8	2.3	52	23	ABP08909	Human OREF protein	165	8	2.3	630	23	AB80765	Geneswitch regulat	
93	8	2.3	60	22	AB83835	Peptide #5861 enco	166	8	2.3	630	23	AB80766	Truncated GAL4 DBD	
94	8	2.3	60	22	AB82532	Protein #5531 enco	167	8	2.3	645	22	AAU25431	Human mdm2 protein	
95	8	2.3	60	22	AA858966	Human brain expres	168	8	2.3	648	21	AA95048	Human mdm2 protein	
96	8	2.3	60	22	AAW71493	Human bone marrow	169	8	2.3	654	23	AB80764	Candida albicans p	
97	8	2.3	60	22	AAW19146	Peptide #580 enco	170	8	2.3	701	23	AB80815	Geneswitch regulat	
98	8	2.3	60	22	AA831794	Peptide #5831 enco	171	8	2.3	773	22	ABG15668	Human cytoskeleton	
99	8	2.3	77	20	AA41590	Human peptide enco	172	8	2.3	796	22	AB857975	Novel human diagno	
100	8	2.3	86	21	AA808968	Arabidopsis thalia	173	8	2.3	797	19	AAW85042	Drosophila melanog	
101	8	2.3	86	21	AA808968	Arabidopsis thalia	174	8	2.3	797	19	AAW85043	PKB-green fluoresc	
102	8	2.3	86	21	AA808968	Arabidopsis thalia	175	8	2.3	797	19	AAW85043	NFKappaB p65 subu	
103	8	2.3	86	22	AB815278	Human nervous syst	176	8	2.3	797	21	AAW70782	EGFP-NFKappaB fusi	
104	8	2.3	90	22	AB871172	Drosophila melanog	177	8	2.3	797	21	AAW70783	NFKappaB-EGFP fusi	
105	8	2.3	100	14	AA842120	Oxalacetate decarb	178	8	2.3	803	22	AAW79014	Human protein SEQ	
106	8	2.3	103	23	AB878540	Ala-Pro-Ala-Pro co	179	8	2.3	805	21	AA822940	GFP-NF-kappa-B fus	
107	8	2.3	120	21	AA822392	Arabidopsis thalia	180	8	2.3	809	21	AA84881	Amino acid sequenc	
108	8	2.3	128	22	AA80159	Human protein SEQ	181	8	2.3	860	21	AA823271	Balanus amphitrite	
109	8	2.3	129	18	AAW14573	Streptococcus pneu	182	8	2.3	891	23	AAO22162	Ramoplanin biosynt	
110	8	2.3	131	21	AA808967	Arabidopsis thalia	183	8	2.3	904	22	AAW79998	Human protein SEQ	
111	8	2.3	131	21	AA808967	Arabidopsis thalia	184	8	2.3	1015	22	AB865826	Drosophila melanog	
112	8	2.3	131	21	AA808967	Arabidopsis thalia	185	8	2.3	1087	22	AA878952	Human cancer-inhib	
113	8	2.3	131	21	AA808967	Arabidopsis thalia	186	8	2.3	1088	20	AA065327	Human WART2, ortho	
114	8	2.3	131	21	AA808967	Arabidopsis thalia	187	8	2.3	1088	21	AA807663	Amino acid sequenc	
115	8	2.3	131	21	AA808967	Arabidopsis thalia	188	8	2.3	1088	21	AA807664	Amino acid sequenc	
116	8	2.3	131	21	AA808967	Arabidopsis thalia	189	8	2.3	1244	22	AA867393	Amino acid sequenc	
117	8	2.3	131	21	AA808967	Arabidopsis thalia	190	8	2.3	1500	22	AB963715	Drosophila melanog	
118	8	2.3	131	21	AA808967	Arabidopsis thalia	191	8	2.3	1698	22	AB867538	Drosophila melanog	
119	8	2.3	131	21	AA808967	Arabidopsis thalia	192	8	2.3	2110	22	AB858077	Drosophila melanog	
120	8	2.3	131	22	AAW14569	Streptococcus pneu	193	8	2.3	2197	21	AA818352	Plasmodium falci	
121	8	2.3	131	22	AA80126	C glutamicum prote	194	7	2.0	3	12	3	AA820015	Protein encoded by
122	8	2.3	131	18	AAW14584	Human mcl-1. Homo	195	7	2.0	13	9	AA808070	Hook region #1 con	
123	8	2.3	197	19	AAW40218	Drosophila melanog	196	7	2.0	14	5	AA808070	Hook region #1 con	
124	8	2.3	202	18	AAW14578	Streptococcus pneu	197	7	2.0	14	7	AA808070	Hook region #1 con	
125	8	2.3	206	18	AAW14574	Streptococcus pneu	198	7	2.0	14	8	AA808070	Hook region #1 con	
126	8	2.3	233	21	AA85188	Streptococcus pneu	199	7	2.0	14	10	AA808070	Hook region #1 con	
127	8	2.3	251	21	AA823248	Oxarl-h1 resistan	200	7	2.0	16	9	AA808070	Hook region #2 con	
128	8	2.3	251	21	AA843170	Arabidopsis thalia	201	7	2.0	16	9	AA808070	Hook region #2 con	
129	8	2.3	254	21	AA823247	Arabidopsis thalia	202	7	2.0	17	14	AA835201	TrpE fragment. Sy	
130	8	2.3	254	21	AA843169	Arabidopsis thalia	203	7	2.0	21	9	AA808070	Hook region #10 co	
131	8	2.3	254	23	AAU72491	Arabidopsis thalia	204	7	2.0	26	23	AB877847	Amino acid sequenc	
132	8	2.3	280	21	AA843168	Arabidopsis thalia	205	7	2.0	35	19	AAW70114	Peptide produced b	
133	8	2.3	281	21	AA823246	Arabidopsis thalia	206	7	2.0	35	22	AAE05575	N-terminal CT6 gly	
134	8	2.3	283	21	AA83088	Arabidopsis thalia	207	7	2.0	35	23	AB877849	Amino acid sequenc	
135	8	2.3	283	22	AAU29681	F-box protein FBP	208	7	2.0	40	19	AAW75737	Flt4 short form am	
136	8	2.3	283	22	AB848300	Novel human secret	209	7	2.0	41	22	AA866551	Human zinc carboxy	
137	8	2.3	284	23	AB890232	Human Zf16 protein	210	7	2.0	42	21	AA866567	Human zinc carboxy	
138	8	2.3	313	22	AAU38739	Human polyptide	211	7	2.0	42	21	AA824882	Arabidopsis thalia	
139	8	2.3	317	22	AAU40791	Streptomyces plica	212	7	2.0	59	9	AA808070	Hook region #3 con	
140	8	2.3	317	22	AAU40792	Human polyptide	213	7	2.0	59	16	AA808070	Hook region #9 con	
141	8	2.3	332	22	AAU17475	Human polyptide	214	7	2.0	60	22	AA873922	B.catarhalis CD e	
142	8	2.3	353	22	AB847447	Novel signal trans	215	7	2.0	61	9	AA825432	Propionibacterium	
143	8	2.3	354	22	AB869632	MOMP P5. Haemophi	216	7	2.0	61	13	AA825432	A leader peptide M	
144	8	2.3	355	16	AA864226	Drosophila melanog	217	7	2.0	61	22	AAU46820	Modified LE leade	
145	8	2.3	355	22	AA865590	Human 38kda FK-506	218	7	2.0	66	16	AAU47772	Propionibacterium	
146	8	2.3	358	21	AA822949	Human FK506-bindin	219	7	2.0	66	16	AAU47772	Human epidermal gr	
147	8	2.3	375	22	AAW79175	Arabidopsis thalia	220	7	2.0	67	16	AAU4528	Peptide encoded by	
148	8	2.3	392	22	AB871846	Human protein SEQ	221	7	2.0	67	21	AAU6908	Peptide MS1-1922.	
149	8	2.3	404	19	AAW68408	Drosophila melanog	222	7	2.0	69	16	AAU47773	Human epidermal gr	
150	8	2.3	437	22	AAU02565	Aujeszky's disease	223	7	2.0	70	18	AAW17660	Stem cell mobilisi	
151	8	2.3	497	21	AAU94523	Angiotensin conver	224	7	2.0	70	23	AAO20015	Human chemokine M	
152	8	2.3	498	21	AAU44562	Mouse diacylglycer	225	7	2.0	70	23	AAO14148	Human MIP-3alpha p	
153	8	2.3	511	22	ABG19496	Mouse diacylglycer	226	7	2.0	73	22	ABG13593	Novel human diagno	
154	8	2.3	516	20	AAU55928	Novel human diagno	227	7	2.0	76	10	AAU90999	Transforming growt	
155	8	2.3	520	20	AAU01496	Human STLK3 protei	228	7	2.0	84	21	AAU00448	Drosophila melanog	
156	8	2.3	520	20	AAU01497	Human pan-s/tk-lb	229	7	2.0	85	20	AAU12719	Human secreted pro	
	8	2.3				Human pan-s/tk-lb	230	7	2.0	87	17	AA895545	HCV II chimeric ep	

230	7	2.0	88	23	ABP03258	Human ORFX protein	303	7	2.0	169	20	AAW89682	Osteogenic fusion
231	7	2.0	89	22	AAG67372	Amino acid sequenc	304	7	2.0	172	14	AAR44753	Osteogenic fusion
232	7	2.0	89	23	ABP11383	Human ORFX protein	305	7	2.0	172	15	AAR51659	Osteogenic fusion
233	7	2.0	90	5	AAW40024	Short fusion prote	306	7	2.0	172	17	AAR85769	CBMP2B1 fusion prot
234	7	2.0	95	19	AAW61279	Exodus protein. H	307	7	2.0	172	19	AAW44309	Human osteogenic f
235	7	2.0	95	21	AAW07939	A human C-C chemok	308	7	2.0	172	20	AAW43120	CBMP2B fusion prot
236	7	2.0	96	17	AAR56690	Liver expressed ch	309	7	2.0	172	20	AAW89686	Osteogenic fusion
237	7	2.0	96	17	AAR93086	Human chemokine be	310	7	2.0	177	20	AAW99644	Hepatitis C virus
238	7	2.0	96	18	AAW22669	Human chemokine be	311	7	2.0	177	21	AAG07298	Arabidopsis thalia
239	7	2.0	96	19	AAW57475	Human chemokine be	312	7	2.0	177	21	AAG53696	Arabidopsis thalia
240	7	2.0	96	19	AAW44308	Human liver and ac	313	7	2.0	177	21	AAW80194	Hepatitis C virus
241	7	2.0	96	20	AAW41103	Human chemokine MI	314	7	2.0	178	22	AAW48072	Human extracellula
242	7	2.0	96	21	AAW97074	Human chemokine be	315	7	2.0	180	21	AAW24658	Plant SDF encoded
243	7	2.0	96	21	AAW95535	Human chemokine MI	316	7	2.0	180	21	AAW24670	Plant SDF encoded
244	7	2.0	96	22	AAW31794	Human chemokine be	317	7	2.0	180	21	AAG59347	Arabidopsis thalia
245	7	2.0	96	23	ABG60667	Amino acid sequenc	318	7	2.0	182	18	AAW32479	Growth factor LHL
246	7	2.0	96	23	AAW019996	Small inducible cy	319	7	2.0	182	20	AAW06907	LHL growth factor
247	7	2.0	96	23	AAW15750	Protein of human c	320	7	2.0	183	21	AAG31245	Arabidopsis thalia
248	7	2.0	98	22	AAG67371	Human chemokine be	321	7	2.0	184	18	AAW14589	Streptococcus pneu
249	7	2.0	101	17	AAR59544	Amino acid sequenc	322	7	2.0	185	18	AAW14566	Streptococcus pneu
250	7	2.0	111	22	ABW39430	HCV I chimeric epi	323	7	2.0	187	21	AAW07573	Protein encoded by
251	7	2.0	111	22	ABW24202	Peptide #6936 enco	324	7	2.0	193	9	AAW08077	Hook region #8 con
252	7	2.0	111	22	AAW60110	Protein #6201 enco	325	7	2.0	209	21	AAG50176	Arabidopsis thalia
253	7	2.0	111	22	AAW72722	Human brain expres	326	7	2.0	212	18	AAW14588	Streptococcus pneu
254	7	2.0	111	22	AAW19703	Human bone marrow	327	7	2.0	212	21	AAG05693	Arabidopsis thalia
255	7	2.0	111	22	AAW32953	Peptide #6137 enco	328	7	2.0	213	18	AAW14587	Streptococcus pneu
256	7	2.0	111	23	ABG42546	Peptide #6990 enco	329	7	2.0	214	22	AAW60079	Streptococcus pneu
257	7	2.0	112	16	AAR74774	Human peptide enco	330	7	2.0	219	21	AAG33440	Human breast cance
258	7	2.0	112	21	AAG42114	Human epidermal gr	331	7	2.0	223	22	ABW67729	Zea mays protein f
259	7	2.0	113	21	AAW50177	Zea mays protein f	332	7	2.0	225	8	AAW70359	Drosophila melanog
260	7	2.0	113	22	AAU04053	Arabidopsis thalia	333	7	2.0	225	8	AAW70061	Sequence encoded b
261	7	2.0	113	22	ABW39444	Propionibacterium	334	7	2.0	227	20	AAW38860	Sequence of human
262	7	2.0	113	22	ABW24209	Peptide #6950 enco	335	7	2.0	227	20	AAW38882	Neisseria meningit
263	7	2.0	113	22	AAW60131	Protein #6208 enco	336	7	2.0	230	4	AAW30210	Sequence of antige
264	7	2.0	113	22	AAW72745	Human brain expres	337	7	2.0	231	22	ABW64660	Sequence of antige
265	7	2.0	113	22	AAW32973	Peptide #7010 enco	338	7	2.0	233	4	AAW30204	Sequence encoded b
266	7	2.0	113	23	ABG42569	Human peptide enco	339	7	2.0	234	4	AAW30209	Sequence of antige
267	7	2.0	117	21	AAG42113	Zea mays protein f	340	7	2.0	234	4	AAW30208	Sequence of antige
268	7	2.0	121	22	AAU16172	Human novel secret	341	7	2.0	235	4	AAW30211	Sequence of antige
269	7	2.0	122	20	AAW38861	Neisseria gonorrh	342	7	2.0	238	18	AAW14587	Streptococcus pneu
270	7	2.0	128	22	ABW30031	Peptide #2682 enco	343	7	2.0	246	21	AAG10846	Arabidopsis thalia
271	7	2.0	128	22	ABW35203	Peptide #2709 enco	344	7	2.0	246	21	AAG45067	Arabidopsis thalia
272	7	2.0	128	22	ABW20644	Protein #2643 enco	345	7	2.0	248	21	AAW10786	Sequence of an FMD
273	7	2.0	128	22	AAW56035	Human brain expres	346	7	2.0	248	21	AAW10786	Arabidopsis thalia
274	7	2.0	128	22	AAW68406	Human bone marrow	347	7	2.0	249	21	AAG47125	Arabidopsis thalia
275	7	2.0	128	22	AAW16221	Peptide #2655 enco	348	7	2.0	251	21	AAG31244	Arabidopsis thalia
276	7	2.0	128	22	AAW28711	Peptide #2748 enco	349	7	2.0	251	21	AAG45066	Arabidopsis thalia
277	7	2.0	128	22	AAW03951	Peptide #2633 enco	350	7	2.0	251	21	AAW77121	Human neurotransm
278	7	2.0	128	22	ABW37979	Human peptide enco	351	7	2.0	252	21	AAG10845	Arabidopsis thalia
279	7	2.0	129	22	ABW96320	Human testicular a	352	7	2.0	252	23	AAU83190	Arabidopsis thalia
280	7	2.0	129	22	AAW59789	Human reproductive	353	7	2.0	255	23	AAU83190	Arabidopsis thalia
281	7	2.0	130	22	AAU59193	Propionibacterium	354	7	2.0	255	23	AAW17482	Human leucine-rich
282	7	2.0	131	21	AAW10847	Arabidopsis thalia	355	7	2.0	258	23	AAW52696	Novel secreted pro
283	7	2.0	131	21	AAG26759	Zea mays protein f	356	7	2.0	260	21	AAW10785	Human myelin prote
284	7	2.0	131	21	AAG45068	Arabidopsis thalia	357	7	2.0	260	21	AAW10785	Arabidopsis thalia
285	7	2.0	133	20	AAW25606	Parietaria sp. all	358	7	2.0	262	5	AAW47124	Arabidopsis thalia
286	7	2.0	134	21	AAG02224	Human secreted pro	359	7	2.0	262	5	AAW47124	Fusion protein con
287	7	2.0	138	20	AAW25610	Parietaria sp. all	360	7	2.0	263	22	ABW08077	Novel human diagno
288	7	2.0	142	22	ABW11242	Human SLIT-2 homol	361	7	2.0	267	22	AAU31012	Novel human secret
289	7	2.0	151	22	ABW17851	Human nervous syst	362	7	2.0	268	21	AAG07297	Arabidopsis thalia
290	7	2.0	155	22	AAU35566	Haemophilus influe	363	7	2.0	268	21	AAG53695	Arabidopsis thalia
291	7	2.0	158	21	AAG42112	Zea mays protein f	364	7	2.0	269	12	AAW11957	Fb-Fb-truncated "
292	7	2.0	159	22	ABW26467	Novel human diagno	365	7	2.0	270	20	AAW43978	Human protein kina
293	7	2.0	165	22	AAG66561	Human secreted met	366	7	2.0	270	20	AAW43979	Human protein kina
294	7	2.0	166	8	AAW70358	Sequence encoded b	367	7	2.0	272	21	AAG43956	Zea mays protein f
295	7	2.0	166	8	AAW70062	Sequence of human	368	7	2.0	276	21	AAG43955	Zea mays protein f
296	7	2.0	166	18	AAW14568	Streptococcus pneu	369	7	2.0	277	20	AAW42775	Rat neuronal limed
297	7	2.0	166	21	AAG26757	Zea mays protein f	370	7	2.0	279	21	AAG07296	Arabidopsis thalia
298	7	2.0	169	14	AAR44749	Osteogenic fusion	371	7	2.0	279	21	AAG53694	Arabidopsis thalia
299	7	2.0	169	15	AAW31655	Osteogenic fusion	372	7	2.0	281	12	AAW11956	Fb-Fb-truncated (6
300	7	2.0	169	17	AAW85765	OP1A fusion protei	373	7	2.0	282	23	AAU95373	Human calcium tran
301	7	2.0	169	19	AAW44305	Human osteogenic f	374	7	2.0	283	22	AAU18235	Novel human DNA-bi
302	7	2.0	169	20	AAW43116	Osteogenic protein	375	7	2.0	284	10	AAW95689	Consensus osteogen
										284	10	AAW95687	CP5 gene product.

376	7	2.0	286	17	AAW03566	Mycobacterium tube	449	7	2.0	405	4	AAP30202	Sequence encoded b
377	7	2.0	288	21	AAV95986	Human zinc finger	450	7	2.0	406	4	AAP30203	Sequence encoded b
378	7	2.0	296	22	ABB65345	Drosophila melanog	451	7	2.0	407	23	ABB92968	Herbicidally activ
379	7	2.0	297	22	ABG27036	Novel human diagno	452	7	2.0	408	14	AAR44752	Osteogenic fusion
380	7	2.0	307	21	AAG43954	Zea mays protein f	453	7	2.0	408	15	AAR51658	Osteogenic fusion
381	7	2.0	310	21	AB14326	Mycobacterium tube	454	7	2.0	408	17	AAR85768	OP1D fusion protei
382	7	2.0	317	14	AAR44750	Osteogenic fusion	455	7	2.0	408	19	AAW44308	Human osteogenic f
383	7	2.0	317	15	AAR51656	Osteogenic fusion	456	7	2.0	408	20	AAV43119	Osteogenic protein
384	7	2.0	317	19	AAW85766	OP1B fusion protei	457	7	2.0	408	20	AAW89685	Osteogenic fusion
385	7	2.0	317	19	AAW44306	Human osteogenic f	458	7	2.0	418	22	ABG03314	Novel human diagno
386	7	2.0	317	20	AAV43117	Osteogenic protein	459	7	2.0	419	14	AAR44754	Osteogenic fusion
387	7	2.0	318	22	AAW89683	Osteogenic fusion	460	7	2.0	419	17	AAR85770	CBMP2B2 fusion pro
388	7	2.0	320	21	AAW56362	Propionibacterium	461	7	2.0	419	19	AAW44310	Human osteogenic f
389	7	2.0	320	21	AAG20559	Arabidopsis thalia	462	7	2.0	419	20	AAV43121	CBMP2B fusion prot
390	7	2.0	322	22	AAU97002	Human CCAAT/enhanc	463	7	2.0	419	20	AAW89687	Osteogenic fusion
391	7	2.0	322	22	AAE11945	Human CCAAT/enhanc	464	7	2.0	421	19	AAW37376	Hepatitis C virus
392	7	2.0	324	21	AAE14143	Bordetella pertuss	465	7	2.0	421	22	ABG67110	Drosophila melanog
393	7	2.0	325	17	AAW03565	Mycobacterium tube	466	7	2.0	424	20	AAV49148	Amino acid sequenc
394	7	2.0	325	21	AAV97281	Fibronectin attach	467	7	2.0	425	20	AAV49147	Amino acid sequenc
395	7	2.0	325	23	AAW50732	Mycobacterium tube	468	7	2.0	426	20	AAV49146	Amino acid sequenc
396	7	2.0	331	22	AB770820	Drosophila melanog	469	7	2.0	428	20	AAW5085	S. pneumoniae resp
397	7	2.0	332	18	AAW32418	Mycobacterium tube	470	7	2.0	428	20	AAW5087	S. pneumoniae resp
398	7	2.0	332	18	AAW32350	Mycobacterium tube	471	7	2.0	429	21	AAG10134	Arabidopsis thalia
399	7	2.0	332	19	AAW81683	M. tuberculosis im	472	7	2.0	429	21	AAG51058	Arabidopsis thalia
400	7	2.0	332	19	AAW64322	Mycobacterium tube	473	7	2.0	431	21	AAG10133	Arabidopsis thalia
401	7	2.0	332	20	AAV39083	M. tuberculosis an	474	7	2.0	431	21	AAG51057	Arabidopsis thalia
402	7	2.0	332	20	AAV38945	M. tuberculosis re	475	7	2.0	437	20	AAV49241	N-terminal region
403	7	2.0	332	22	AAU01895	M. tuberculosis re	476	7	2.0	437	20	AAV49244	N-terminal region
404	7	2.0	332	23	AAE17584	M. tuberculosis DP	477	7	2.0	437	20	AAV32180	N-terminal choline
405	7	2.0	337	21	AAV74311	Mycobacterium spec	478	7	2.0	437	20	AAV32183	N-terminal choline
406	7	2.0	342	23	AAE22547	Neisseria gonorrhe	479	7	2.0	439	20	AAV49240	N-terminal choline
407	7	2.0	345	12	AAE14408	CTAI-DD fusion pro	480	7	2.0	439	20	AAV32179	N-terminal choline
408	7	2.0	345	22	AAU97001	Nuclear factor C/E	481	7	2.0	444	23	AAE24240	Human 23566 (carbo
409	7	2.0	345	22	AAE11944	Human CCAAT/enhanc	482	7	2.0	453	16	AAE23918	CD protein of Bran
410	7	2.0	345	22	AAU09068	Human transcriptio	483	7	2.0	477	22	ABW59024	Drosophila melanog
411	7	2.0	345	23	AAO15441	Human C/EBP-beta p	484	7	2.0	477	22	AAU18155	Novel human DNA-bi
412	7	2.0	345	23	AAO15442	Human C/EBP-beta p	485	7	2.0	478	22	ABG02907	Novel human diagno
413	7	2.0	345	23	AAO15443	Human C/EBP-beta m	486	7	2.0	484	14	AAR44751	Osteogenic fusion
414	7	2.0	345	23	AAO15449	Human C/EBP-beta p	487	7	2.0	484	15	AAR51657	Osteogenic fusion
415	7	2.0	345	23	AAO15450	Human C/EBP-beta m	488	7	2.0	484	17	AAR85767	OP1C fusion protei
416	7	2.0	345	23	AAO15451	Human C/EBP-beta m	489	7	2.0	484	19	AAW44307	Human osteogenic f
417	7	2.0	345	23	AAO15452	Human C/EBP-beta p	490	7	2.0	484	20	AAV43118	Osteogenic protein
418	7	2.0	345	23	AAO15453	Human C/EBP-beta m	491	7	2.0	484	20	AAW89684	Osteogenic fusion
419	7	2.0	345	23	AAO15454	Human C/EBP-beta m	492	7	2.0	508	16	AAW80631	Osteogenic fusion
420	7	2.0	345	23	AAU97259	Human C/EBP-beta p	493	7	2.0	512	22	ABG1369	2B10 AMH-receptor
421	7	2.0	345	23	AAU97260	Human alternative	494	7	2.0	569	16	AAW80632	Drosophila melanog
422	7	2.0	345	23	AAU97261	Human alternative	495	7	2.0	574	22	AAW52322	H1 AMH-receptor
423	7	2.0	345	23	AAU97262	Human type human C/	496	7	2.0	574	22	AAW52322	WASP homolog prote
424	7	2.0	345	23	AAU97263	Human C/EBP-beta pr	497	7	2.0	574	22	AAW52322	Amino acid sequenc
425	7	2.0	345	23	AAU97264	Human C/EBP-beta pr	498	7	2.0	576	22	ABW61241	Drosophila melanog
426	7	2.0	345	23	AAU97265	Human C/EBP-beta pr	499	7	2.0	587	22	ABW61241	Pseudomonas aerugi
427	7	2.0	345	23	AAU97266	Human C/EBP-beta pr	500	7	2.0	593	19	AAW61912	Human blue-light p
428	7	2.0	345	23	AAU97267	Human C/EBP-beta pr	501	7	2.0	594	22	ABW61362	Drosophila melanog
429	7	2.0	345	23	AAU97268	Human C/EBP-beta pr	502	7	2.0	609	4	AAP30206	Sequence encoded b
430	7	2.0	348	16	AAW49182	Human C/EBP-beta	503	7	2.0	617	22	AAU09073	Mouse sphingosine
431	7	2.0	350	23	AAW85938	Protein tyrosine-k	504	7	2.0	631	22	AAW83274	Chlamydia trachoma
432	7	2.0	350	23	ABW38388	Herbicidally activ	505	7	2.0	631	23	ABW94245	Chlamydia trachoma
433	7	2.0	354	22	ABW62869	Arabidopsis thalia	506	7	2.0	640	22	AAE07167	Mycobacterium tube
434	7	2.0	354	22	AAW66560	Drosophila melanog	507	7	2.0	652	20	AAV39225	M. tuberculosis fus
435	7	2.0	354	22	AAW66566	Human secreted met	508	7	2.0	652	20	AAV39082	M. tuberculosis fus
436	7	2.0	362	22	AAW74682	Human secreted met	509	7	2.0	663	23	ABW3753	Herbicidally activ
437	7	2.0	366	23	ABW91952	Human protease and	510	7	2.0	677	22	AAU21657	Novel human neopla
438	7	2.0	367	13	AAW27244	Herbicidally activ	511	7	2.0	723	22	AAW93529	Human polypeptide
439	7	2.0	371	22	AAW08079	Sequence encoded b	512	7	2.0	723	22	AAW93529	Human polypeptide
440	7	2.0	374	22	AAW66547	Novel human diagno	513	7	2.0	729	23	AAW19849	Mycobacterium tube
441	7	2.0	374	22	AAW66565	Human secreted met	514	7	2.0	729	23	AAU70957	M. tuberculosis Rv
442	7	2.0	374	22	AAW66566	Human secreted met	515	7	2.0	733	22	AAW93424	Human polypeptide
443	7	2.0	380	15	AAW51660	Amino acid sequenc	516	7	2.0	733	22	AAW93852	Human polypeptide
444	7	2.0	388	22	AAW66813	Osteogenic fusion	517	7	2.0	802	19	AAW81746	M. tuberculosis fu
445	7	2.0	390	22	ABW70754	Drosophila melanog	518	7	2.0	802	19	AAW64379	M. tuberculosis fu
446	7	2.0	394	21	AAG10135	Drosophila melanog	519	7	2.0	802	20	AAV32063	Mycobacterium anti
447	7	2.0	394	21	AAW51059	Arabidopsis thalia	520	7	2.0	802	20	AAV39224	Mycobacterium tube
448	7	2.0	399	22	ABW64411	Arabidopsis thalia	521	7	2.0	802	20	AAV39176	M. tuberculosis fu
						Drosophila melanog				802	20	AAV39081	M. tuberculosis fu

522	7	2.0	802	20	AAU39033	M. tuberculosis fu	595	7	2.0	2665	22	AAU66665	Human bone marrow
523	7	2.0	802	23	AAU74592	Antigenic fusion p	596	7	2.0	2665	22	AAU14533	Peptide #967 encod
524	7	2.0	811	22	ABG62661	Drosophila melanog	597	7	2.0	2665	22	AAU26950	Peptide #987 encod
525	7	2.0	852	20	AAU31246	Murine raIGDS prot	598	7	2.0	2665	22	AAU02259	Peptide #941 encod
526	7	2.0	852	20	AAU30948	Human E3 ubiquitin	599	7	2.0	2665	23	ABG36319	Human peptide enco
527	7	2.0	852	21	AAU23176	Human raIGDS (hral	600	7	2.0	3192	22	AAE10128	Streptomyces nous
528	7	2.0	854	20	AAU30949	Murine E3 ubiquiti	601	7	2.0	3266	21	AAU42491	Human ORFX ORF2255
529	7	2.0	883	22	AAU80136	Human protein SEQ	602	7	2.0	3536	22	ABG65480	Drosophila melanog
530	7	2.0	903	22	AAU37116	Protein involved i	603	7	2.0	8	10	AAU91876	Peptide sequence o
531	7	2.0	919	22	AAU79152	Human polypeptide	604	6	1.7	8	22	AAU26860	Human Leukocyte An
532	7	2.0	931	22	AAU39815	Human polypeptide	605	6	1.7	8	22	AAU26860	p53 epitope B7 sup
533	7	2.0	937	23	ABP30468	Streptococcus poly	606	6	1.7	8	22	AAU89654	p53 epitope B7 sup
534	7	2.0	948	23	ABP27191	Human macrophage c	607	6	1.7	8	22	AAU89655	Tumour associated
535	7	2.0	972	23	AAU79039	Human macrophage c	608	6	1.7	8	22	AAU76065	Tumour associated
536	7	2.0	972	23	AAU11934	Colony stimulating	609	6	1.7	9	17	AAU97524	Antigenic peptide,
537	7	2.0	972	23	AAU11935	Colony stimulating	610	6	1.7	9	21	AAU54192	HLA binding peptid
538	7	2.0	972	23	AAU11936	Colony stimulating	611	6	1.7	9	22	AAU26579	Human Leukocyte An
539	7	2.0	972	23	AAU11937	Colony stimulating	612	6	1.7	9	22	AAU89387	p53 DR supermotif
540	7	2.0	972	23	AAU11938	Colony stimulating	613	6	1.7	10	17	AAU97522	Antigenic peptide,
541	7	2.0	972	23	AAU11939	Colony stimulating	614	6	1.7	10	17	AAU89375	p53 derived immuno
542	7	2.0	972	23	AAU11940	Colony stimulating	615	6	1.7	10	22	AAU26915	Human Leukocyte An
543	7	2.0	972	23	AAU11941	Colony stimulating	616	6	1.7	10	22	AAU89641	p53 epitope B7 sup
544	7	2.0	972	23	AAU11942	Colony stimulating	617	6	1.7	10	22	AAU00619	MUCL competition b
545	7	2.0	972	23	AAU73585	Colony stimulating	618	6	1.7	10	22	AAU76201	Tumour associated
546	7	2.0	975	22	AAE07144	Mutant murine Kit/	619	6	1.7	10	22	AAU76202	Tumour associated
547	7	2.0	976	22	AAE07148	Mutant murine Kit/	620	6	1.7	10	22	AAU76202	Tumour associated
548	7	2.0	976	22	AAE07149	Human Kit/stem cel	621	6	1.7	11	14	AAU44263	p53 derived HLA an
549	7	2.0	976	22	AAU00375	Human stem cell gr	622	6	1.7	11	14	AAU44263	Residues 68-78 of
550	7	2.0	977	21	AAU51322	Bovine c-Kit bk-1	623	6	1.7	11	17	AAU97523	Antigenic peptide,
551	7	2.0	1016	22	AAU38901	C. trachomatis CT8	624	6	1.7	11	23	AAU48400	Ribosome binding s
552	7	2.0	1021	19	AAU76192	Actinoplanes sp. a	625	6	1.7	11	23	AAU48400	Ribosome binding s
553	7	2.0	1021	23	AAU49562	Actinoplanes sp. a	626	6	1.7	12	12	AAU93084	Portion of Bacillu
554	7	2.0	1023	23	AAU82954	Human homologue of	627	6	1.7	12	16	AAU80038	Tri operon partial
555	7	2.0	1039	22	ABG69116	Drosophila melanog	628	6	1.7	12	22	AAU98707	Human peptide #198
556	7	2.0	1055	22	ABG15479	Novel human diago	629	6	1.7	13	12	AAU12478	"Hydrophobic tail"
557	7	2.0	1058	23	ABP41533	Human ovarian anti	630	6	1.7	13	15	AAU49993	Peptide analogue o
558	7	2.0	1130	20	AAU13446	Human aortic carbo	631	6	1.7	13	21	AAU52528	House dust mite al
559	7	2.0	1158	23	AAE22739	Human adipocyte en	632	6	1.7	13	23	AAU52528	Der HMW-map polype
560	7	2.0	1243	22	ABG21221	Novel human diago	633	6	1.7	14	19	AAU79130	Sequence present i
561	7	2.0	1265	23	AAE22546	CTAL-OVA-DD fusion	634	6	1.7	14	22	AAU98340	Human peptide #161
562	7	2.0	1298	16	AAE5937	Protein tyrosine-k	635	6	1.7	15	17	AAU99956	Bacillus thuringie
563	7	2.0	1298	17	AAU90528	Flt4 receptor tyro	636	6	1.7	15	18	AAU38913	Peptide resembling
564	7	2.0	1298	21	AAU30542	Amino acid sequenc	637	6	1.7	15	21	AAU65514	Oestrogen receptor
565	7	2.0	1298	21	AAU90365	Human Flt4 recepto	638	6	1.7	15	22	AAU89437	p53 DR supermotif
566	7	2.0	1298	22	AAU70746	Human tyrosine kin	639	6	1.7	15	23	AAU86251	Soybean diverged d
567	7	2.0	1298	22	AAU97575	Mouse Flt-4 protei	640	6	1.7	17	23	AAU20560	GHR binding H5 pep
568	7	2.0	1298	22	AAU97575	Human Flt4 recepto	641	6	1.7	17	23	AAU20560	GHR binding H5 pep
569	7	2.0	1363	21	AAU90366	Human Flt4 recepto	642	6	1.7	18	23	ABP48134	Human cytomagalovi
570	7	2.0	1363	21	AAU90366	Human tyrosine kin	643	6	1.7	18	23	ABP48134	HHV8 ORF K8.1-der1
571	7	2.0	1363	21	AAU70747	Human Flt4 recepto	644	6	1.7	18	23	ABP48134	HHV8 ORF K8.1-der1
572	7	2.0	1363	22	AAU37604	Human tyrosine kin	645	6	1.7	20	20	AAU05756	HHV8 ORF K8.1-der1
573	7	2.0	1406	21	AAU42916	Human ORFX ORF2680	646	6	1.7	20	21	AAU58503	HHV8 ORF K8.1-der1
574	7	2.0	1444	22	ABG15667	Novel human diago	647	6	1.7	20	21	AAU58516	HHV8 ORF K8.1-der1
575	7	2.0	1464	22	ABG15667	Novel human diago	648	6	1.7	20	21	AAU58516	HHV8 ORF K8.1-der1
576	7	2.0	1487	23	AAU14351	Drosophila melanog	649	6	1.7	20	21	AAU58518	HHV8 ORF K8.1-der1
577	7	2.0	1487	23	AAU14352	Equine herpesvirus	650	6	1.7	20	21	AAU58518	HHV8 ORF K8.1-der1
578	7	2.0	1487	23	AAU14353	Equine herpesvirus	651	6	1.7	20	21	AAU58518	HHV8 ORF K8.1-der1
579	7	2.0	1487	23	AAU14334	Equine herpesvirus	652	6	1.7	20	21	AAU58518	HHV8 ORF K8.1-der1
580	7	2.0	1487	23	AAU14335	Equine herpesvirus	653	6	1.7	20	21	AAU58518	HHV8 ORF K8.1-der1
581	7	2.0	1487	23	AAU14335	Equine herpesvirus	654	6	1.7	20	21	AAU58518	HHV8 ORF K8.1-der1
582	7	2.0	1618	13	AAU27205	Human nestin. Hom	655	6	1.7	20	21	AAU58530	HHV8 ORF K8.1-der1
583	7	2.0	1618	15	AAU60127	Human nestin. Hom	656	6	1.7	20	21	AAU58530	HHV8 ORF K8.1-der1
584	7	2.0	1618	22	AAU3898	Nestin polypeptide	657	6	1.7	21	19	AAU42513	Peptide derived fr
585	7	2.0	1693	22	ABG58927	Drosophila melanog	658	6	1.7	21	25	AAU30526	Peptide fragment o
586	7	2.0	1909	22	ABG19127	Novel human diago	659	6	1.7	25	22	AAU30526	Insert A to preven
587	7	2.0	2129	22	ABG15478	Novel human diago	660	6	1.7	28	13	AAU27561	Human cytomagalovi
588	7	2.0	2129	22	ABG20749	Novel human diago	661	6	1.7	30	14	AAU33088	Delta6-16.0(delta6
589	7	2.0	2220	21	AAU42235	Human ORFX ORF199	662	6	1.7	30	21	AAU15194	Delta6-16.0(delta6
590	7	2.0	2220	21	AAU54004	Full length calcin	663	6	1.7	30	21	AAU15194	Delta6-16.0(delta6
591	7	2.0	2658	22	ABG28314	Human peptide #965	664	6	1.7	30	21	AAU15198	Delta6-16.0(delta6
592	7	2.0	2665	22	ABG33490	Peptide #996 encod	665	6	1.7	31	14	AAU33086	Human cytomagalovi
593	7	2.0	2665	22	ABG18950	Protein #949 encod	666	6	1.7	31	14	AAU33087	Human cytomagalovi
594	7	2.0	2665	22	AAU54270	Human brain expres	667	6	1.7	31	21	AAU58498	HHV8 ORF K8.1 dom1

6	1.7	32	14	AAR33089	Human cytomegalovi	741	73	22	AAW86639	Human immune/haem
6	1.7	33	21	AAW44695	Human secreted pro	742	74	19	AAW40436	Tobacco invertase
6	1.7	34	13	AAR27562	Insert B to preven	743	74	21	AAW91020	Mouse OBM protein
6	1.7	34	19	AAW48443	Human p53 prolina-	744	74	22	AAW91020	Protonibacterium
6	1.7	34	21	AAW58504	HHV8 ORF K8.1 b1va	745	76	21	AAW61732	Human pancreatic c
6	1.7	35	14	AAR33083	Human cytomegalovi	746	76	22	AAW54024	Protonibacterium
6	1.7	35	21	AAW22929	Arabidopsis thalia	747	76	22	AAW62682	C glutaminc prote
6	1.7	38	21	AAG57714	Arabidopsis thalia	748	76	22	AAW91916	Plant SDF encoded
6	1.7	40	21	AAG20091	Arabidopsis thalia	749	78	21	AAW24990	Plant SDF encoded
6	1.7	41	14	AAR33090	Human cytomegalovi	750	78	21	AAW25095	Novel human diagno
6	1.7	41	14	AAR33092	Human cytomegalovi	751	81	22	ABG28149	Human death domain
6	1.7	41	14	AAR33092	Human cytomegalovi	752	81	22	ABG28149	Human ORFX protein
6	1.7	42	19	AAW42515	Peptide #2229 enco	753	83	22	ABP04105	Drosophila melanog
6	1.7	42	22	ABW29611	Peptide #2262 enco	754	83	22	ABW68958	Arabidopsis thalia
6	1.7	42	22	ABW34793	Peptide #2299 enco	755	85	21	AAW44488	Protonibacterium
6	1.7	42	22	ABW20208	Protein #2207 enco	756	85	22	AAW37573	Arabidopsis thalia
6	1.7	42	22	AAW55591	Human brain expres	757	85	22	AAW59296	Protonibacterium
6	1.7	42	22	AAW67977	Human bone marrow	758	85	22	AAW67776	Human foetal prote
6	1.7	42	22	AAW15795	Peptide #2229 enco	759	86	21	AAW21205	Arabidopsis thalia
6	1.7	42	22	AAW28304	Peptide #2341 enco	760	86	22	AAW59180	Protonibacterium
6	1.7	42	22	AAW03530	Peptide #2212 enco	761	87	21	AAW93410	Amino acid sequenc
6	1.7	42	23	ABG37514	Human peptide enco	762	87	22	ABW69259	Drosophila melanog
6	1.7	43	20	AAW14020	YhdD repeat sequen	763	87	22	AAW60382	Protonibacterium
6	1.7	49	22	AAW82269	Human immune/haema	764	88	21	AAW61758	Arabidopsis thalia
6	1.7	50	23	ABP32396	Human ORF1369 prot	765	88	23	ABP33218	Human ORF2191 prot
6	1.7	50	23	ABP32754	Human ORF1727 prot	766	89	19	AAW98257	Human ORF3334 prot
6	1.7	51	14	AAR33091	Human cytomegalovi	767	89	22	ABW69512	H. pylori GHPO 176
6	1.7	52	21	AAW05444	Arabidopsis thalia	768	90	16	AAW80185	Drosophila melanog
6	1.7	52	21	AAW33693	Arabidopsis thalia	769	90	22	AAE10715	Mispl-derived poly
6	1.7	53	22	AAW04413	Human polypeptide	770	90	22	AAE10715	Human 4ST3GALP do
6	1.7	57	21	AAW19720	Arabidopsis thalia	771	90	22	AAE10717	Mouse 4ST3GALP do
6	1.7	57	21	AAW61016	Arabidopsis thalia	772	92	21	AAW58986	Pig 4ST3GALP doma
6	1.7	57	22	AAW40796	Protonibacterium	773	93	21	AAW32637	Amino acid sequenc
6	1.7	57	22	AAW66718	Protonibacterium	774	93	21	AAW32637	Breast and ovarian
6	1.7	58	22	ABW40042	Peptide #7548 enco	775	93	22	ABW30898	Eucalyptus grandis
6	1.7	58	22	ABW24544	Protein #6543 enco	776	93	22	ABW36080	Peptide #3549 enco
6	1.7	58	22	AAW60792	Human brain expres	777	93	22	ABW21472	Peptide #3586 enco
6	1.7	58	22	AAW73467	Human bone marrow	778	93	22	AAW56862	Human brain expres
6	1.7	58	22	AAW19975	Peptide #6409 enco	779	93	22	AAW69249	Human bone marrow
6	1.7	58	22	AAW33665	Peptide #7702 enco	780	93	22	AAW17078	Peptide #3512 enco
6	1.7	58	23	ABW43326	Human peptide enco	781	93	22	AAW29572	Peptide #3609 enco
6	1.7	59	23	ABP11087	Human ORFX protein	782	93	22	AAW04779	Peptide #3461 enco
6	1.7	62	21	AAW45407	Human secreted pro	783	93	23	ABG38859	Human peptide enco
6	1.7	62	22	AAU66864	Protonibacterium	784	94	21	AAW59219	Arabidopsis thalia
6	1.7	62	22	AAU54552	Protonibacterium	785	95	21	AAW52703	Arabidopsis thalia
6	1.7	63	21	AAG20090	Arabidopsis thalia	786	95	22	AAW57703	Protonibacterium
6	1.7	63	21	AAG03612	Arabidopsis thalia	787	95	22	AAW86608	Human immune/haema
6	1.7	63	22	AAW81132	Human secreted pro	788	97	22	AAW37572	Arabidopsis thalia
6	1.7	63	23	AAE11026	Hepatitis B virus	789	97	21	AAW43179	Protonibacterium
6	1.7	64	23	ABP11025	Hepatitis B virus	790	98	22	AAW69550	Drosophila melanog
6	1.7	65	22	AAU48572	Human ORFX protein	791	101	22	AAW65875	Protonibacterium
6	1.7	65	23	ABP10274	Human ORFX protein	792	102	22	AAW43619	Polypeptide isolat
6	1.7	67	23	AAE17028	C-terminally trunc	793	102	22	AAW72875	Protonibacterium
6	1.7	68	21	AAW59221	Human immune/haema	794	103	22	AAW63289	Human p53 A76T/V12
6	1.7	68	22	AAW84291	Arabidopsis thalia	795	103	22	AAW09338	Protonibacterium
6	1.7	68	22	AAW81134	Hepatitis B virus	796	104	21	AAW09338	Protonibacterium
6	1.7	68	23	ABP10544	Hepatitis B virus	797	104	21	AAW39764	Arabidopsis thalia
6	1.7	69	21	AAW59220	Human ORFX protein	798	104	22	AAW01073	Arabidopsis thalia
6	1.7	69	22	AAU17820	Arabidopsis thalia	799	105	16	AAW80084	Human polypeptide
6	1.7	70	9	AAW80077	Novel human respir	800	105	16	AAW80084	Mouse derived heav
6	1.7	70	21	AAW26198	Cytomegalovirus (C	801	105	16	AAW80084	Mouse derived heav
6	1.7	70	22	ABG02382	Arabidopsis thalia	802	105	20	AAW36869	Amino acid sequenc
6	1.7	70	22	AAW72000	Novel human diagno	803	105	21	AAW19719	Arabidopsis thalia
6	1.7	71	22	AAW12538	P. funiculosus aci	804	105	21	AAW61014	Arabidopsis thalia
6	1.7	72	21	AAW24991	Human polypeptide	805	105	22	ABG25066	Novel human diagno
6	1.7	72	21	AAW25096	Plant SDF encoded	806	107	16	AAW94314	Mouse derived heav
6	1.7	72	22	ABW67912	Plant SDF encoded	807	107	16	AAW94314	Lactococcus lactis
6	1.7	72	22	AAW64454	Drosophila melanog	808	108	23	ABW55374	Drosophila melanog
6	1.7	72	22	ABG26938	Protonibacterium	809	109	22	AAU31460	Novel human secret
6	1.7	73	21	AAW42000	Novel human diagno	810	109	22	AAW25600	Human protein sequ
6	1.7	73	21	AAW03301	Arabidopsis thalia	811	111	22	AAW94756	Human ORFX protein
6	1.7	73	22	ABW68706	Human secreted pro	812	112	23	ABP05668	Human ORFX protein
6	1.7	73	22	ABG25702	Drosophila melanog	813	113	19	AAW60153	M. vaccae antigen
6	1.7	73	22	ABG25702	Novel human diagno	813	113	20	AAW14900	M. vaccae antigen

814	1.7	113	20	AAU36969	Amino acid sequenc	887	6	1.7	140	22	AAU20102	Human liver associ
815	1.7	113	23	AAU78277	Human RNA cyclase	888	6	1.7	140	23	ABP40963	Human liver associ
816	1.7	113	23	ABP73506	M vaccae GV-42 pro	889	6	1.7	141	13	AAU22999	Cell adhesio inhi
817	1.7	114	7	AAU60286	Sequence of pre-S(890	6	1.7	141	13	AAU22999	Cell adhesio inhi
818	1.7	114	10	AAU94770	ayw pre-S1 sequenc	891	6	1.7	141	22	ABG13837	Arabidopsis thalia
819	1.7	114	21	AAU30585	A human variable l	892	6	1.7	141	22	ABG13837	Drosophila thalia
820	1.7	116	16	AAU80187	MISPI-derived poly	893	6	1.7	142	22	AAU05029	Human polypeptide
821	1.7	116	16	AAU80189	MISPI-derived poly	894	6	1.7	143	18	AAU09017	Immunogenic type F
822	1.7	116	21	AAU37425	Human secreted pro	895	6	1.7	143	22	ABG04424	Novel human diagno
823	1.7	116	21	AAU37426	Human secreted pro	896	6	1.7	143	22	ABG04424	Novel human diagno
824	1.7	117	22	AAU80206	Human autoantibody	897	6	1.7	143	22	ABG11775	Novel human diagno
825	1.7	117	22	AAU32011	Novel human secret	898	6	1.7	143	22	ABG25379	Novel human diagno
826	1.7	118	21	AAU53493	Human colon cancer	899	6	1.7	144	13	AAU23000	Novel human diagno
827	1.7	118	22	AAU01269	Human polypeptide	900	6	1.7	144	22	AAU19986	Cell adhesio inhi
828	1.7	119	21	AAU73472	Human secreted pro	901	6	1.7	145	22	ABG05153	Human camelio 3 (H
829	1.7	119	21	AAU65432	Human 5' ESR relat	902	6	1.7	145	22	ABG05153	Human camelio 3 (H
830	1.7	119	22	AAU65431	Protonibacterium	903	6	1.7	147	21	AAU19118	Novel human diagno
831	1.7	120	22	AAU43965	Protonibacterium	904	6	1.7	147	21	AAU19118	Novel human diagno
832	1.7	120	22	AAU43965	Protonibacterium	905	6	1.7	148	21	AAU19118	Polypeptide isolat
833	1.7	121	22	ABG27743	Novel human diagno	906	6	1.7	151	22	AAU31846	Arabidopsis thalia
834	1.7	121	22	ABG27743	Escherichia coli p	907	6	1.7	152	21	AAU45064	Human p53 W91C/C12
835	1.7	121	22	ABG27743	Human interleukin	908	6	1.7	153	20	AAU74188	D. immitis aromati
836	1.7	121	22	AAU02146	Human polypeptide	909	6	1.7	153	21	AAU74188	Human prostate tum
837	1.7	121	23	AAU74499	Human polypeptide	910	6	1.7	154	19	AAU72396	Arabidopsis thalia
838	1.7	122	21	AAU41997	Human polypeptide	911	6	1.7	154	21	AAU37571	Pathogen response
839	1.7	122	22	ABG68984	Drosophila melanog	912	6	1.7	154	22	ABG01354	Arabidopsis thalia
840	1.7	122	22	AAU22040	Human cardiovascu	913	6	1.7	155	22	AAU94097	Novel human diagno
841	1.7	122	22	AAU811517	Human p27 protein	914	6	1.7	156	21	AAU08872	Human protein sequ
842	1.7	122	22	AAU51103	Human p27 protein	915	6	1.7	156	21	AAU08872	Arabidopsis thalia
843	1.7	122	22	AAU59168	165 gene homologo	916	6	1.7	156	21	AAU60211	Arabidopsis thalia
844	1.7	124	18	AAU17362	Human p27. Homo s	917	6	1.7	156	21	AAU60211	Arabidopsis thalia
845	1.7	124	18	AAU14582	Streptococcus pneu	918	6	1.7	157	21	AAU60665	Arabidopsis thalia
846	1.7	124	21	AAU12104	Arabidopsis thalia	919	6	1.7	158	16	AAU82701	Arabidopsis thalia
847	1.7	125	7	AAU60285	Sequence of pre-S(920	6	1.7	158	18	AAU13870	Rice fungal resist
848	1.7	125	10	AAU94769	adw Pre-S1 sequenc	921	6	1.7	159	22	AAU67370	Protein encoded by
849	1.7	125	20	AAU90283	Human anti-GPIIb/I	922	6	1.7	159	22	ABG20855	Protonibacterium
850	1.7	125	22	AAU73577	Human colon cancer	923	6	1.7	159	23	ABG77704	Novel human diagno
851	1.7	127	22	AAU01736	Human polypeptide	924	6	1.7	160	21	AAU18461	Amino acid sequenc
852	1.7	128	21	AAU09850	Arabidopsis thalia	925	6	1.7	161	21	AAU44887	Arabidopsis thalia
853	1.7	129	21	AAU44495	Plant viral moveme	926	6	1.7	161	21	AAU44887	Zea mays protein f
854	1.7	129	22	AAU39842	Protonibacterium	927	6	1.7	162	18	AAU17050	Blackcurrant Rib1
855	1.7	130	21	AAU85182	Protonibacterium	928	6	1.7	162	21	AAU08871	Arabidopsis thalia
856	1.7	131	23	AAU014583	Barley Rarl fragme	929	6	1.7	162	21	AAU60215	Arabidopsis thalia
857	1.7	131	18	AAU15671	Ribosomal protein	930	6	1.7	162	22	ABG15181	Arabidopsis thalia
858	1.7	131	21	AAU15672	Streptococcus pneu	931	6	1.7	162	23	ABG97844	Novel human diagno
859	1.7	131	21	AAU15672	Gene 1 human secre	932	6	1.7	163	22	AAU45596	Human secretory po
860	1.7	131	21	AAU60290	Human secreted pro	933	6	1.7	164	21	AAU56873	Protonibacterium
861	1.7	131	21	AAU02651	Arabidopsis thalia	934	6	1.7	164	21	AAU56873	Human prostate can
862	1.7	131	22	ABG66658	Human secreted pro	935	6	1.7	164	21	AAU60209	Arabidopsis thalia
863	1.7	131	22	AAU09514	Drosophila melanog	936	6	1.7	164	21	AAU60214	Arabidopsis thalia
864	1.7	132	19	AAU75070	Human polypeptide	937	6	1.7	164	21	AAU93740	Arabidopsis thalia
865	1.7	132	23	AAU75352	Human secreted pro	938	6	1.7	164	21	AAU93740	Amino acid sequenc
866	1.7	133	22	ABG60260	Human octamer bind	939	6	1.7	165	14	AAU42838	Hepatitis B virus
867	1.7	133	22	AAU43804	Human ovarian anti	940	6	1.7	165	20	AAU08302	Prothymosin N term
868	1.7	133	22	AAU44998	Protonibacterium	941	6	1.7	166	21	AAU58502	Mouse odorant bind
869	1.7	133	22	AAU44998	Protonibacterium	942	6	1.7	166	21	AAU58502	Arabidopsis thalia
870	1.7	133	22	AAU25765	Human reproductive	943	6	1.7	167	22	AAU23656	HHV8 ORF K8.1b pro
871	1.7	133	22	AAU35197	Human protein sequ	944	6	1.7	167	23	ABP34591	Novel human enzyme
872	1.7	133	22	AAU19874	Human transmembran	945	6	1.7	168	18	AAU24127	Human kinase-like
873	1.7	133	23	ABG61731	Human novel extrac	946	6	1.7	168	21	AAU09925	Pyrococcus proteas
874	1.7	133	23	ABP48094	Human polypeptide	947	6	1.7	168	22	AAU33944	Arabidopsis thalia
875	1.7	136	21	AAU09937	Arabidopsis thalia	948	6	1.7	169	22	AAU41662	Staphylococcus aur
876	1.7	136	21	AAU33199	Arabidopsis thalia	949	6	1.7	170	22	ABG02214	Protonibacterium
877	1.7	136	21	AAU33199	Zea mays protein f	950	6	1.7	170	22	AAU33099	Novel human diagno
878	1.7	137	22	AAU01761	Arabidopsis thalia	951	6	1.7	171	21	AAU42103	Human polypeptide
879	1.7	138	21	AAU09849	Arabidopsis thalia	952	6	1.7	172	21	AAU45056	Human OREF ORF1867
880	1.7	138	23	ABU49190	Human secreted pro	953	6	1.7	172	23	ABP04807	D. immitis aromati
881	1.7	139	21	AAU09936	Listeria monocytog	954	6	1.7	173	18	AAU17035	Human OREF protein
882	1.7	139	21	AAU39762	Arabidopsis thalia	955	6	1.7	173	21	AAU40419	Blackcurrant fruit
883	1.7	139	22	AAU1184	Arabidopsis thalia	956	6	1.7	173	22	ABG58786	Zea mays protein f
884	1.7	140	18	AAU22493	Mycobacterium tube	957	6	1.7	173	22	AAU36793	Drosophila thalia
885	1.7	140	22	AAU66261	Phaffia derived gl	958	6	1.7	173	22	AAU37229	Staphylococcus aur
886	1.7	140	22	AAU93094	Protonibacterium	959	6	1.7	173	22	AAU37542	Staphylococcus aur

Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTQAG 344

RESULT 6 AA93341

ID AA93341 standard; Protein; 344 AA.

AC AA93341;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of a Klebsiella P40 protein.

XX P40 protein; outer membrane protein A; OmpA; antigen-presenting cell;
KW dendritic cell; antigen delivery; immune response; cancer;
KW tumour-associated antigen; autoimmune disease; allergy; graft rejection;
KW cardiovascular disease; central nervous system disease; inflammation;
KW infection; immune deficiency.

OS Klebsiella pneumoniae.

XX WO200027432-A1.

PN 18-MAY-2000.

XX 08-NOV-1999; 99WO-FR02734.

XX 06-NOV-1998; 98FR-0014007.

XX (FABR) FABRE MEDICAMENT SA PIERRE.

XX Bonnefoy J, Lecoanet S, Aubry J, Jeannin P, Baussant T;

XX WPI; 2000-387342/33.

DR N-PSDB; AA15498.

XX Use of enterobacterial outer membrane protein A for delivering active
PT substances, particularly immunogens for treating or preventing e.g.
PT cancer, to antigen presenting cells

PS Claim 9; Page 28-29; 35pp; French.

XX The present sequence represents a P40 protein. The protein is an
CC outer membrane protein A (OmpA). The protein is used in pharmaceutical
CC compositions for specific targeting of an active substance to
CC antigen-presenting cells (APCs), especially dendritic cells. OmpA binds
CC specifically to APCs and is internalised by them (in contrast to other
CC protein carriers such as tetanus toxoid). The OmpA protein is used to
CC deliver an antigen or hapten to modify (specifically to improve) an
CC immune response, especially for treatment or prevention of cancers
CC (particularly those that express a associated-associated antigen),
CC autoimmune disease, allergy, graft rejection, cardiovascular or
CC central nervous system diseases, inflammation, infection or immune
CC deficiency.

XX Sequence 344 AA;

Query Match 100.0%; Score 344; DB 21; Length 344;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAIFVLAAPKDNNTWYAGKLGWSQYHDTGYNGFQNNNGPTRNDQLGAGFGGYQVN 60
DB 1 MKAIFVLAAPKDNNTWYAGKLGWSQYHDTGYNGFQNNNGPTRNDQLGAGFGGYQVN 60

QY 61 PYLGFEMGYDNLGRMAYKGSVDNGAFKAGQVOLTAKLGYPTDLDIYTRLGGMWWRADS 120
DB 61 PYLGFEMGYDNLGRMAYKGSVDNGAFKAGQVOLTAKLGYPTDLDIYTRLGGMWWRADS 120

QY 121 KGNVASTGVSRSSEHDTGVSFVAGGVENAVTDTATRLLEYQWNNIGDAGVGTGTPDNGM 180
DB 121 KGNVASTGVSRSSEHDTGVSFVAGGVENAVTDTATRLLEYQWNNIGDAGVGTGTPDNGM 180

QY 181 LSLGVSYRFGQEDAAPVAPAPAPAPAPATKHFHTLKSDFLNFENKATLKPEGOALDOLY 240
DB 181 LSLGVSYRFGQEDAAPVAPAPAPAPAPATKHFHTLKSDFLNFENKATLKPEGOALDOLY 240
QY 241 TOLSNMDDPKGSASVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPACKISARGMGE 300
DB 241 TOLSNMDDPKGSASVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPACKISARGMGE 300
QY 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTQAG 344
DB 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTQAG 344

RESULT 7

AA63698

ID AA63698 standard; Protein; 344 AA.

XX AA63698;

DT 29-OCT-2001 (first entry)

DE Amino acid sequence of an outer membrane protein A, P40.

XX Outer membrane protein A; P40; antigen presenting cell; vaccine;
KW antiviral; antibacterial; anticancer; autoimmune disease; inflammation;
KW graft rejection; cardiovascular disease; immune deficiency.

OS Klebsiella pneumoniae.

XX FR2803302-A1.

XX 06-JUL-2001.

XX 04-JAN-2000; 2000FR-0000070.

XX 04-JAN-2000; 2000FR-0000070.

XX (FABR) FABRE MEDICAMENT SA PIERRE.

XX Baussant T, Jeannin P, Delneste Y, Lawny F, Bonnefoy JY;

XX WPI; 2001-427232/46.

XX N-PSDB; AAH74731.

XX Preparing purified polypeptide soluble in absence of detergent, useful
PT for modulating the immune system, e.g. in vaccines, by removal of
PT detergent, denaturing and molecular sieving

PS Claim 9; Page 24-25; 34pp; French.

XX The present sequence represents an outer membrane protein A (P40) of
CC Klebsiella pneumoniae. The protein is soluble in aqueous solvent in
CC absence of detergent. The specification describes a method for the
CC preparation of this polypeptide. The P40 protein binds selectively to
CC antigen-presenting cell, so provides targeting, proliferation and/or
CC expression of molecules by these cells. P40 is used, alone or as an
CC adjuvant, to produce therapeutic compositions that are soluble in
CC absence of detergent, especially when formulated with an antigen or
CC hapten for modulating the host's immune system. Especially, it is used
CC to prepare vaccines, especially antiviral, antibacterial or anticancer
CC (e.g. against human immune deficiency virus, respiratory syncytial virus,
CC measles, mumps, tuberculosis etc.), but also against fungi, parasites,
CC autoimmune diseases, graft rejection, cardiovascular disease,
CC inflammation and immune deficiency.

XX Sequence 344 AA;

Query Match 100.0%; Score 344; DB 22; Length 344;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAIFVLAAPKDNNTWYAGKLGWSQYHDTGYNGFQNNNGPTRNDQLGAGFGGYQVN 60
DB 1 MKAIFVLAAPKDNNTWYAGKLGWSQYHDTGYNGFQNNNGPTRNDQLGAGFGGYQVN 60

RESULT	10
AAW47796	
ID	AAW47796 standard; protein; 344 AA.
XX	
AC	AAW47796;
XX	
DT	01-MAR-2002 (first entry)
XX	
DE	Klebsiella pneumoniae OmpA protein.
XX	
KW	OmpA; enterobacterium; antibacterial; antifungal; antiviral;
KW	antiparasitic; antimicrobial; infection.
XX	
OS	Klebsiella pneumoniae.
XX	
PN	WO200187326-A1.
PD	22-NOV-2001.
XX	
PF	16-MAY-2001; 2001WO-FR01490.
XX	
PR	16-MAY-2000; 2000FR-0006199.
XX	
PA	(FABR) FABRE MEDICAMENT SA PIERRE.
XX	
PI	Jeannin P, Delneste Y, Baussant T;
XX	
DR	WPI; 2002-055641/07.
XX	
PT	Use of an enterobacterium OmpA protein for prophylactic and therapeutic
PT	treatment of viral, bacterial, fungal and parasitic infections -
PS	Claim 8; Page 24-25; 33pp; French.
XX	
CC	The present sequence is OmpA protein from enterobacteria Klebsiella
CC	pneumoniae. OmpA protein can be used to prepare an antimicrobial
CC	pharmaceutical composition for mucosal delivery. The composition can be
CC	used for prophylactic and therapeutic treatment of viral, bacterial,
CC	fungal and parasitic infections.
XX	
SQ	Sequence 344 AA;
Query Watch	100.0%; Score 344; DB 23; Length 344;
Best Local Similarity	100.0%; Pred.. No. 0;
Matches 344; Conservative	0; Mismatches 0; Indels 0; Gaps-
QY	1 MKAIFVLNAPKONTWWAGGKLGSQHVDTFGVNGFQNNGPTRNDQLGAGAFGGYQVN 60

CC and zoonosis caused by Salmonella of the same serogroup. The carrier
 CC proteins enhance the immunogenicity of the oligo- or polysaccharide
 CC antigens. Inclusion of additional Salmonella capsule antigens, such as
 CC the Vi antigen, increases the vaccine's efficacy against encapsulated
 CC bacteria. The present sequence, protein LP40, is a preferred example of
 CC a carrier protein which can be used in the immunocomplex. It is
 CC obtained by recombinant expression of a modified kieb. pneumoniae I-145
 CC p40 gene in E. coli.
 XX
 SQ Sequence 344 AA;

Query Match 99.4%; Score 342; DB 18; Length 344;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
 DB 1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
 QY 61 PYLGFEMGYDMLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWVRADS 120
 DB 61 PYLGFEMGYDMLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWVRADS 120
 QY 121 KGNVASTGVSSEHDTGSPVFAGGVAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGM 180
 DB 121 KGNVASTGVSSEHDTGSPVFAGGVAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGM 180
 QY 181 LSLGVSRYFGQEDAAVPVAP 240
 DB 181 LSLGVSRYFGQEDAAVPVAP 240
 QY 241 TQLSNMDPKDGSVAVLGYTRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300
 DB 241 TQLSNMDPKDGSVAVLGYTRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300
 QY 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGKEVVTOP 342
 DB 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGKEVVTOP 342

RESULT 12
 AAY44077
 ID AAY44077 standard; Protein; 344 AA.
 AC AAY44077;
 DT 18-JAN-2000 (first entry)
 XX K.pneumoniae OmpA protein.
 DE Outer membrane protein; ompA; enterobacterium; Klebsiella pneumoniae;
 KW immunity; mammal; antigen; haptgen; infection; human; bovine;
 KW respiratory syncytial virus; protective response.
 XX Klebsiella pneumoniae.

OS FR2776521-A1.
 XX
 PN 01-OCT-1999.
 XX
 PD 27-MAR-1998; 98FR-0003814.
 XX
 PF 27-MAR-1998; 98FR-0003814.
 XX
 PR 27-MAR-1998; 98FR-0003814.
 XX
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 PA Andreoni C, Rauli I, Nguyen TN, Haeuw JF, Baussant T;
 XX WPI: 1999-583089/50.
 XX N-PSDB; AAZ30477.
 XX
 PT Immunogenic composition containing bacterial outer membrane protein
 PT conjugated or fused to antigen or haptgen, for nasal administration, to

PT protect against respiratory pathogens -
 XX Claim 1; Page 17-18; 64pp; French.
 PS
 XX
 CC The invention relates to the use of a fragment of a bacterial membrane
 CC protein, especially the outer membrane protein from an enterobacterium,
 CC e.g. the OmpA protein from Klebsiella pneumoniae, in a composition for
 CC nasal administration to improve immunity, in mammals, against an antigen
 CC or haptgen. The antigen or haptgen is derived from bacteria and viruses
 CC that cause respiratory infections e.g. the human or bovine respiratory
 CC syncytial virus. This sequence corresponds to the OmpA protein from
 CC Klebsiella. The antigens are shown in AAY44078-Y44149 (AAZ30478-330538
 CC for coding sequences). The use of a membrane protein, from a species
 CC other than that from which the antigen is derived, induces a protective
 CC response against the antigen, even without an adjuvant, since most
 CC adults will already be sensitized against the membrane protein, although
 CC the membrane protein-antigen product will induce an anti-membrane
 CC protein response even in subjects who are not pre-sensitized.
 XX
 SQ Sequence 344 AA;

Query Match 99.4%; Score 342; DB 20; Length 344;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
 DB 1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
 QY 61 PYLGFEMGYDMLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWVRADS 120
 DB 61 PYLGFEMGYDMLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWVRADS 120
 QY 121 KGNVASTGVSSEHDTGSPVFAGGVAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGM 180
 DB 121 KGNVASTGVSSEHDTGSPVFAGGVAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGM 180
 QY 181 LSLGVSRYFGQEDAAVPVAP 240
 DB 181 LSLGVSRYFGQEDAAVPVAP 240
 QY 241 TQLSNMDPKDGSVAVLGYTRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300
 DB 241 TQLSNMDPKDGSVAVLGYTRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300
 QY 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGKEVVTOP 342
 DB 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGKEVVTOP 342

RESULT 13
 AAG67743
 ID AAG67743 standard; Protein; 344 AA.
 AC AAG67743;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Amino acid sequence of a Klebsiella protein.
 XX
 KW zwitterionic detergent; Immune response; vaccine; IgA production;
 KW IGG response; tumour; viral infection; bacterial infection;
 KW parasitic infection.
 XX
 OS Klebsiella pneumoniae.
 XX
 PN FR2805163-A1.
 XX
 PD 24-AUG-2001..
 XX
 PF 21-FEB-2000; 2000FR-0002104.
 XX
 PR 21-FEB-2000; 2000FR-0002104.

XX PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX PI Goestch L, Corvaia N, Beck A, Haeuw JF;
 XX DR WPI; 2001-591759/67.
 XX DR N-PSDB; AAH78461.
 XX PT Mucosally administered vaccines containing zwitterionic detergents to
 PT induce or improve immune response towards antigen or haptens, especially
 PT used in antibacterial, antiviral, antiparasitic or antitumor vaccines
 PT
 XX PS Disclosure; Page 21-22; 26pp; French.
 XX CC The present sequence represents a Klebsiella protein. The protein is
 CC administered to test the adjuvant effect of zwitterionic detergents.
 CC The specification describes the use of zwitterionic detergents in the
 CC preparation of a mucosally administered pharmaceutical composition for
 CC inducing or improving the immune response of a mammal towards an antigen
 CC or hapten. In presence of zwitterionic detergents, vaccines are
 CC effective on mucosal (especially nasal) administration, which has the
 CC general advantages of inducing specific IgA production directly at the
 CC site of infection, stimulating a systemic IgG-type response (creating a
 CC secondary barrier against infection) and being simpler to carry out
 CC than administration by injection. The pharmaceutical composition is
 CC specifically a vaccine for the treatment or prophylaxis of tumours or
 CC viral, bacterial or parasitic infections.
 XX CC
 XX SQ Sequence 344 AA;
 Query Match 99.4%; Score 342; DB 22; Length 344;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKAIFVLNAAPKDNWTYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
 DB 1 MKAIFVLNAAPKDNWTYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
 QY 61 PYLGFEMGYDNLGRMAYKGSVDNGAFKAQGVLTAKLGYPTDDLDIYTRLGGMVWRADS 120
 DB 61 PYLGFEMGYDNLGRMAYKGSVDNGAFKAQGVLTAKLGYPTDDLDIYTRLGGMVWRADS 120
 QY 121 KGNVASTGVSRSEHDTGVSFVAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGM 180
 DB 121 KGNVASTGVSRSEHDTGVSFVAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGM 180
 QY 181 LSLGVSRYRFGQEDAAPVAP 240
 DB 181 LSLGVSRYRFGQEDAAPVAP 240
 QY 241 TOLSNMDDPKDGSVAVLYGTYDRIGSEAYNQOLSEKRAQSVVDVLYVAKGIPAGKISARGMGE 300
 DB 241 TOLSNMDDPKDGSVAVLYGTYDRIGSEAYNQOLSEKRAQSVVDVLYVAKGIPAGKISARGMGE 300
 QY 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
 DB 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
 RESULT 14
 ID AAB84122
 XX AAB84122 standard; Protein; 344 AA.
 AC AAB84122;
 XX 06-AUG-2001 (first entry)
 XX Amino acid sequence of a recombinant outer membrane protein A (rp40).
 DE Outer membrane protein A; rp40; OMP; enterobacterium; nasal vaccine;
 KW respiratory tract pathogen.
 XX

OS Klebsiella pneumoniae.
 XX FR2801219-A1.
 PN XX
 PI XX
 PD 25-MAY-2001.
 XX
 PF 18-SEP-2000; 2000FR-0011862.
 XX
 PR 27-MAR-1998; 98FR-0003814.
 XX
 PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX
 PI Andreoni C, Raully I, Nguyen T, Haeuw JF, Bausant T;
 XX WPI; 2001-358083/38.
 DR N-PSDB; AAF90077.
 XX
 PT Recombinant production of a protein, for particularly use as a carrier
 PT protein in nasal vaccines, comprises renaturation, after extraction, in
 PT the presence of specific detergents
 XX
 PS Claim 8; Page 26-27; 48pp; French.
 XX
 CC The present sequence represents a recombinant outer membrane protein A,
 CC designated rp40. The specification describes a method for the
 CC recombinant production of a protein, or its fragments. The method
 CC comprises renaturation of the protein, after extraction, in the presence of
 CC a solution containing one of the detergents Zwittergent 3-14,
 CC Zwittergent 3-12 and octylglucopyranoside, where the protein is not
 CC beta-interferon. The protein is especially the outer membrane protein
 CC (OMP) from an enterobacterium, and is useful as a carrier for delivering
 CC antigens or haptens in a nasal vaccine formulation, particularly directed
 CC against pathogens of the respiratory tract, e.g. respiratory syncytial
 CC virus (RSV), (para)influenza, hanta virus, Streptococci, Pneumococci
 CC and Meningococci, especially human or bovine RSV. Most adults show an
 CC antibody response to the Klebsiella pneumoniae p40, and this
 CC sensitisation stimulates the immune response to an antigen/hapten
 CC conjugated to the protein.
 XX
 XX SQ Sequence 344 AA;
 Query Match 99.4%; Score 342; DB 22; Length 344;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKAIFVLNAAPKDNWTYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
 DB 1 MKAIFVLNAAPKDNWTYAGGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
 QY 61 PYLGFEMGYDNLGRMAYKGSVDNGAFKAQGVLTAKLGYPTDDLDIYTRLGGMVWRADS 120
 DB 61 PYLGFEMGYDNLGRMAYKGSVDNGAFKAQGVLTAKLGYPTDDLDIYTRLGGMVWRADS 120
 QY 121 KGNVASTGVSRSEHDTGVSFVAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGM 180
 DB 121 KGNVASTGVSRSEHDTGVSFVAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGM 180
 QY 181 LSLGVSRYRFGQEDAAPVAP 240
 DB 181 LSLGVSRYRFGQEDAAPVAP 240
 QY 241 TOLSNMDDPKDGSVAVLYGTYDRIGSEAYNQOLSEKRAQSVVDVLYVAKGIPAGKISARGMGE 300
 DB 241 TOLSNMDDPKDGSVAVLYGTYDRIGSEAYNQOLSEKRAQSVVDVLYVAKGIPAGKISARGMGE 300
 QY 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
 DB 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
 RESULT 15
 ID AAB67771
 ID AAB67771 standard; Protein; 452 AA.

XX AAB6771;
AC 11-JUN-2001 (first entry)
XX
XX
DE Amino acid sequence of a fusion protein of P40 and RSV antigen.
XX
XX
KW Outer membrane protein A; OmpA; P40; enterobacteria; nasal composition;
KW RSV; RSV infection; lung; respiratory tract; vaccine.
XX
OS Synthetic.
OS Klebsiella pneumoniae.
OS Respiratory syncytial virus.
XX
PN WO200121203-A1.
XX
XX
PD 29-MAR-2001.
XX
XX
PF 22-SEP-2000; 2000WO-FR02626.
XX
XX
PR 23-SEP-1999; 99FR-0011888.
XX
XX
PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX
PI Corvatea N, Goestch L;
XX
XX
DR WPI; 2001-257929/26.
DR N-PSDB; AAF80153.
XX
XX
PT Vaccine against respiratory syncytial virus, comprises enterobacterial
PT outer membrane protein and viral immunogen, provides protective
PT response throughout the respiratory tract.

XX Example 2; Page 31-32; 39pp; French.

XX The present sequence represents a fusion protein comprising a Klebsiella
CC pneumoniae outer membrane protein A (OmpA) designated P40 and a
CC respiratory syncytial virus (RSV) antigen. Enterobacterium OmpA proteins,
CC associated with an immunogenic peptide from RSV are used to prepare
CC a nasal composition that induces a protective response, against RSV
CC infection in the upper and lower (lung) respiratory tract. OmpA
CC potentiates the immune response to some immunogenic peptides,
CC eliminating the need for adjuvants. The method is useful for producing
CC vaccines for prevention or treatment of RSV infections.
XX
XX
SQ Sequence 452 AA;

Query Match 99.4%; Score 342; DB 22; Length 452;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKAIFVLNAPKDNWYAGKLGHSQYHDTGFCYNGFQNNNGPTRNDOLGAGAFGGYQVN 60
Db 1 MKAIFVLNAPKDNWYAGKLGHSQYHDTGFCYNGFQNNNGPTRNDOLGAGAFGGYQVN 60
Qy 61 PYLGFEMGYDNLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWRADS 120
Db 61 PYLGFEMGYDNLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWRADS 120
Qy 121 KGNVASTGVSRSRSHDTCVSPVAGGVEMAVTRDIATRLFYQWNNIGDAGTGTFRDNGM 180
Db 121 KGNVASTGVSRSRSHDTCVSPVAGGVEMAVTRDIATRLFYQWNNIGDAGTGTFRDNGM 180
Qy 181 LSLGVSYRFGQEDAAPVAP 240
Db 181 LSLGVSYRFGQEDAAPVAP 240
Qy 241 TQLSNMDPKDGSVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300
Db 241 TQLSNMDPKDGSVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300
Qy 301 SNPVTGNTCDNVKARAALIDCLAPDRREVEIEVKYKEVVTQP 342
|||||

Db 301 SNPVTGNTCDNVKARAALIDCLAPDRREVEIEVKYKEVVTQP 342

Search completed: April 15, 2003, 08:55:13
Job time : 64 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 08:54:09 ; Search time 15 Seconds
(without alignments)
674.766 Million cell updates/sec

Title: US-09-831-061-2
Perfect score: 344
Sequence: 1 MKAIFVLAAPKONTWYAGG.....DRRVEIEVKGYKEVITQPAG 344

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 5

Total number of hits satisfying chosen parameters: 6183

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	335	97.4	335	4	US-08-836-500A-2
2	179	52.0	179	4	US-08-836-500A-4
3	72	20.9	72	4	US-08-836-500A-6
4	53	15.4	53	4	US-08-836-500A-8
5	10	2.9	359	1	US-08-457-9978-2
6	10	2.9	359	3	US-08-467-722A-2
7	9	2.6	338	1	US-08-210-394-1
8	9	2.6	594	3	US-08-826-964-2
9	8	2.3	26	3	US-08-920-610-10
10	8	2.3	100	6	5252466-19
11	8	2.3	165	1	US-07-956-700B-106
12	8	2.3	165	1	US-08-476-537-106
13	8	2.3	165	1	US-08-485-607-106
14	8	2.3	165	2	US-08-473-879-106
15	8	2.3	165	4	US-09-433-043B-106
16	8	2.3	170	4	US-09-433-043B-127
17	8	2.3	197	1	US-08-690-095-5
18	8	2.3	197	3	US-09-113-789-5
19	8	2.3	404	4	US-09-203-468A-8
20	8	2.3	498	4	US-09-103-734A-5
21	8	2.3	537	3	US-08-920-610-2
22	8	2.3	550	5	PCT-US93-03027-1
23	8	2.3	719	4	US-08-765-907A-15
24	8	2.3	805	4	US-09-513-783A-178
25	7	2.0	35	4	US-09-001-984C-11
26	7	2.0	35	4	US-09-001-984C-42
27	7	2.0	40	4	US-08-795-430-4
28	7	2.0	40	4	US-08-510-133A-8
29	7	2.0	40	4	US-08-585-895-8
30	7	2.0	40	4	US-09-355-700-4
31	7	2.0	40	4	US-08-601-132-8
32	7	2.0	59	1	US-08-306-871-25
33	7	2.0	59	1	US-08-569-959-25
34	7	2.0	61	1	US-08-095-898-6
35	7	2.0	61	5	PCT-US92-09439-6
36	7	2.0	67	2	US-08-142-551B-9
37	7	2.0	95	3	US-08-970-403-2
38	7	2.0	96	1	US-08-347-492B-4
39	7	2.0	96	2	US-08-798-143-4
40	7	2.0	96	2	US-08-458-355A-2
41	7	2.0	96	4	US-08-613-822-2
42	7	2.0	96	4	US-09-479-729B-2
43	7	2.0	96	4	US-09-496-273-2
44	7	2.0	96	4	US-09-261-201A-2
45	7	2.0	96	5	PCT-US95-15484-4
46	7	2.0	140	2	US-08-501-195-1
47	7	2.0	169	1	US-07-841-646-9
48	7	2.0	169	1	US-08-147-023-9
49	7	2.0	169	1	US-08-447-570-9
50	7	2.0	169	2	US-08-449-700-9
51	7	2.0	169	2	US-08-449-699A-9
52	7	2.0	172	1	US-07-841-646-17
53	7	2.0	172	1	US-08-147-023-17
54	7	2.0	172	1	US-08-447-570-17
55	7	2.0	172	2	US-08-449-700-17
56	7	2.0	172	2	US-08-449-699A-17
57	7	2.0	182	3	US-08-828-741B-2
58	7	2.0	182	4	US-09-160-587-2
59	7	2.0	270	2	US-07-857-224B-77
60	7	2.0	270	2	US-07-857-224B-78
61	7	2.0	286	1	US-08-382-184-3
62	7	2.0	286	2	US-08-641-356-3
63	7	2.0	286	4	US-09-132-528-4
64	7	2.0	286	4	US-08-875-494-3
65	7	2.0	286	4	US-09-539-366-4
66	7	2.0	286	4	US-08-875-494-3
67	7	2.0	286	4	US-09-492-985-2
68	7	2.0	310	3	US-08-796-792-4
69	7	2.0	317	1	US-07-841-646-11
70	7	2.0	317	1	US-08-147-023-11
71	7	2.0	317	1	US-08-447-570-11
72	7	2.0	317	2	US-08-449-700-11
73	7	2.0	317	2	US-08-449-699A-11
74	7	2.0	325	1	US-08-382-184-2
75	7	2.0	325	2	US-08-641-356-2
76	7	2.0	325	4	US-09-132-528-2
77	7	2.0	325	4	US-09-132-528-3
78	7	2.0	325	4	US-08-875-494-2
79	7	2.0	325	4	US-09-539-366-2
80	7	2.0	325	4	US-09-539-366-3
81	7	2.0	325	4	US-08-875-494-2
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83	7	2.0	332	4	US-08-818-111-53
84	7	2.0	332	4	US-09-056-556-53
85	7	2.0	332	4	US-09-072-596-53
86	7	2.0	337	2	US-08-861-464-12
87	7	2.0	337	2	US-08-396-001-12
88	7	2.0	337	4	US-09-323-433A-12
89	7	2.0	348	1	US-08-222-616-18
90	7	2.0	348	4	US-08-446-648-18
91	7	2.0	348	5	PCT-US95-04228-18
92	7	2.0	361	4	US-08-874-569B-21
93	7	2.0	367	1	US-08-257-341-5
94	7	2.0	408	1	US-07-841-646-15
95	7	2.0	408	1	US-08-147-023-15
96	7	2.0	408	1	US-08-447-570-15
97	7	2.0	408	2	US-08-449-700-15
98	7	2.0	408	2	US-08-449-699A-15
99	7	2.0	419	1	US-07-841-646-19
100	7	2.0	419	1	US-08-147-023-19

101	7	2.0	1	US-08-447-570-19	Sequence 19, Appl	174	6	1.7	29	4	US-08-894-139-12	Sequence 12, Appl
102	7	2.0	419	US-08-449-700-19	Sequence 19, Appl	175	6	1.7	30	1	US-08-460-874A-14	Sequence 14, Appl
103	7	2.0	419	US-08-449-699A-19	Sequence 19, Appl	176	6	1.7	30	2	US-08-388-883B-14	Sequence 14, Appl
104	7	2.0	421	US-09-020-846-68	Sequence 68, Appl	177	6	1.7	30	4	US-08-462-211A-14	Sequence 14, Appl
105	7	2.0	428	US-09-139-064-2	Sequence 2, Appl	178	6	1.7	31	1	US-08-460-874A-12	Sequence 12, Appl
106	7	2.0	428	US-09-139-064-4	Sequence 4, Appl	179	6	1.7	31	1	US-08-460-874A-13	Sequence 13, Appl
107	7	2.0	428	US-09-487-370-2	Sequence 2, Appl	180	6	1.7	31	2	US-08-388-883B-12	Sequence 12, Appl
108	7	2.0	428	US-09-487-370-4	Sequence 4, Appl	181	6	1.7	31	2	US-08-388-883B-13	Sequence 13, Appl
109	7	2.0	433	US-08-810-116-9	Sequence 9, Appl	182	6	1.7	31	4	US-08-462-211A-12	Sequence 12, Appl
110	7	2.0	433	US-07-930-548A-9	Sequence 9, Appl	183	6	1.7	31	4	US-08-462-211A-13	Sequence 13, Appl
111	7	2.0	437	US-08-810-116-10	Sequence 10, Appl	184	6	1.7	32	1	US-08-460-874A-15	Sequence 15, Appl
112	7	2.0	437	US-07-930-548A-10	Sequence 10, Appl	185	6	1.7	32	2	US-08-388-883B-15	Sequence 15, Appl
113	7	2.0	484	US-07-841-646-13	Sequence 13, Appl	186	6	1.7	32	4	US-08-462-211A-15	Sequence 15, Appl
114	7	2.0	484	US-08-147-023-13	Sequence 13, Appl	187	6	1.7	34	6	5514582-28	Patent No. 5514582
115	7	2.0	484	US-08-447-570-13	Sequence 13, Appl	188	6	1.7	35	1	US-08-460-874A-9	Sequence 9, Appl
116	7	2.0	484	US-08-449-700-13	Sequence 13, Appl	189	6	1.7	35	2	US-08-388-883B-9	Sequence 9, Appl
117	7	2.0	484	US-08-449-699A-13	Sequence 13, Appl	190	6	1.7	35	4	US-08-462-211A-9	Sequence 9, Appl
118	7	2.0	582	US-08-906-865-3	Sequence 3, Appl	191	6	1.7	36	2	US-08-388-883B-16	Sequence 16, Appl
119	7	2.0	582	US-09-129-668-3	Sequence 3, Appl	192	6	1.7	38	4	US-08-826-134-28	Sequence 28, Appl
120	7	2.0	593	US-08-964-268-2	Sequence 2, Appl	193	6	1.7	41	1	US-08-388-883B-1	Sequence 1, Appl
121	7	2.0	631	US-09-620-412C-325	Sequence 325, App	194	6	1.7	41	1	US-08-460-874A-16	Sequence 16, Appl
122	7	2.0	640	US-09-177-349-4	Sequence 4, Appl	195	6	1.7	41	2	US-08-388-883B-18	Sequence 18, Appl
123	7	2.0	652	US-09-072-596-350	Sequence 350, App	196	6	1.7	41	2	US-08-462-211A-16	Sequence 16, Appl
124	7	2.0	802	US-09-056-556-214	Sequence 214, App	197	6	1.7	41	4	US-08-462-211A-18	Sequence 18, Appl
125	7	2.0	802	US-09-072-596-209	Sequence 209, App	198	6	1.7	42	4	US-08-826-134-17	Sequence 17, Appl
126	7	2.0	852	US-08-408-519-5	Sequence 5, Appl	199	6	1.7	48	1	US-08-062-472B-47	Sequence 47, Appl
127	7	2.0	852	US-09-070-060-3	Sequence 3, Appl	200	6	1.7	51	1	US-08-460-874A-17	Sequence 17, Appl
128	7	2.0	852	PCT-US95-03552-5	Sequence 5, Appl	201	6	1.7	51	2	US-08-388-883B-17	Sequence 17, Appl
129	7	2.0	854	US-09-070-060-4	Sequence 4, Appl	202	6	1.7	51	5	US-08-462-211A-17	Sequence 17, Appl
130	7	2.0	854	US-09-357-746-3	Sequence 3, Appl	203	6	1.7	51	6	5198542-13	Patent No. 5198542
131	7	2.0	854	US-09-070-060-4	Sequence 4, Appl	204	6	1.7	51	6	US-08-209-747-16	Sequence 16, Appl
132	7	2.0	854	US-09-357-746-4	Sequence 4, Appl	205	6	1.7	90	1	US-08-458-298-16	Sequence 16, Appl
133	7	2.0	972	US-08-750-141A-2	Sequence 2, Appl	206	6	1.7	90	1	US-09-334-601-23	Sequence 23, Appl
134	7	2.0	976	US-08-750-141A-1	Sequence 1, Appl	207	6	1.7	90	4	US-09-334-601-24	Sequence 24, Appl
135	7	2.0	1158	US-09-060-482-2	Sequence 2, Appl	208	6	1.7	90	4	US-09-334-601-25	Sequence 25, Appl
136	7	2.0	1298	US-08-222-616-33	Sequence 33, Appl	209	6	1.7	90	4	US-09-383-586-34	Sequence 34, Appl
137	7	2.0	1298	US-08-340-011-2	Sequence 2, Appl	210	6	1.7	102	4	US-08-997-080-140	Sequence 140, App
138	7	2.0	1298	US-08-901-710-2	Sequence 33, Appl	211	6	1.7	113	2	US-08-997-362-140	Sequence 140, App
139	7	2.0	1298	US-08-446-648-33	Sequence 33, Appl	212	6	1.7	113	2	US-09-095-855-140	Sequence 140, App
140	7	2.0	1298	PCT-US95-04228-33	Sequence 33, Appl	213	6	1.7	113	4	US-09-324-542-140	Sequence 140, App
141	7	2.0	1362	US-08-874-678-33	Sequence 33, Appl	214	6	1.7	113	4	US-09-205-426-140	Sequence 140, App
142	7	2.0	1362	US-08-643-839-33	Sequence 33, Appl	215	6	1.7	113	4	US-08-480-173A-52	Sequence 52, Appl
143	7	2.0	1362	US-09-348-886-33	Sequence 33, Appl	216	6	1.7	114	3	US-08-484-408A-52	Sequence 52, Appl
144	7	2.0	1363	US-08-340-011-4	Sequence 4, Appl	217	6	1.7	114	3	US-08-209-747-18	Sequence 18, Appl
145	7	2.0	1363	US-08-874-678-32	Sequence 32, Appl	218	6	1.7	116	1	US-08-458-298-18	Sequence 18, Appl
146	7	2.0	1363	US-08-643-839-32	Sequence 32, Appl	219	6	1.7	116	1	US-08-487-748A-17	Sequence 17, Appl
147	7	2.0	1363	US-08-901-710-4	Sequence 32, Appl	220	6	1.7	122	1	US-08-716-588-3	Sequence 3, Appl
148	7	2.0	1363	US-09-348-886-32	Sequence 32, Appl	221	6	1.7	122	2	US-08-966-444-3	Sequence 3, Appl
149	7	2.0	1368	US-08-874-678-34	Sequence 34, Appl	222	6	1.7	122	3	US-08-398-633-17	Sequence 17, Appl
150	7	2.0	1368	US-08-643-839-34	Sequence 34, Appl	223	6	1.7	122	3	US-08-829-525-17	Sequence 17, Appl
151	7	2.0	1368	US-09-348-886-34	Sequence 34, Appl	224	6	1.7	122	3	US-08-609-583A-17	Sequence 17, Appl
152	7	2.0	1618	US-07-853-913-4	Sequence 4, Appl	225	6	1.7	122	4	US-08-937-399-17	Sequence 17, Appl
153	6	1.7	6	US-08-748-073-2	Sequence 2, Appl	226	6	1.7	122	4	US-09-310-367-17	Sequence 17, Appl
154	6	1.7	6	US-08-766-596A-46	Sequence 46, Appl	227	6	1.7	122	4	US-08-480-173A-50	Sequence 50, Appl
155	6	1.7	7	US-08-766-596A-45	Sequence 45, Appl	228	6	1.7	122	4	US-08-484-408A-50	Sequence 50, Appl
156	6	1.7	9	PCT-US95-16415-19	Sequence 19, Appl	229	6	1.7	125	3	US-09-091-725-45	Sequence 45, Appl
157	6	1.7	11	US-08-338-634-8	Sequence 8, Appl	230	6	1.7	125	3	US-09-383-586-35	Sequence 35, Appl
158	6	1.7	11	PCT-US95-16415-18	Sequence 18, Appl	231	6	1.7	140	4	US-08-460-874A-33	Sequence 33, Appl
159	6	1.7	12	US-08-460-874A-46	Sequence 46, Appl	232	6	1.7	147	4	US-08-388-883B-33	Sequence 33, Appl
160	6	1.7	12	US-08-388-883B-46	Sequence 46, Appl	233	6	1.7	162	1	US-08-462-211A-33	Sequence 33, Appl
161	6	1.7	12	US-08-462-211A-46	Sequence 46, Appl	234	6	1.7	162	2	US-09-068-140A-2	Sequence 2, Appl
162	6	1.7	12	US-09-027-998A-47	Sequence 47, Appl	235	6	1.7	170	2	US-08-683-262B-49	Sequence 49, Appl
163	6	1.7	13	US-09-292-225-29	Sequence 29, Appl	236	6	1.7	170	4	US-09-361-707-49	Sequence 49, Appl
164	6	1.7	15	US-08-602-998A-309	Sequence 309, App	237	6	1.7	170	4	US-09-068-140A-13	Sequence 13, Appl
165	6	1.7	15	US-09-027-998A-3	Sequence 3, Appl	238	6	1.7	170	4	US-08-683-262B-42	Sequence 42, Appl
166	6	1.7	15	US-09-500-124-309	Sequence 309, App	239	6	1.7	173	4	US-08-683-262B-43	Sequence 43, Appl
167	6	1.7	18	US-08-990-888-25	Sequence 25, Appl	240	6	1.7	174	2	US-08-683-262B-45	Sequence 45, Appl
168	6	1.7	18	US-08-990-888-28	Sequence 28, Appl	241	6	1.7	174	2	US-08-683-262B-46	Sequence 46, Appl
169	6	1.7	18	US-08-990-888-65	Sequence 65, Appl	242	6	1.7	174	2	US-08-683-262B-47	Sequence 47, Appl
170	6	1.7	20	US-08-935-009A-5	Sequence 5, Appl	243	6	1.7	174	2	US-08-683-262B-48	Sequence 48, Appl
171	6	1.7	21	US-08-460-874A-35	Sequence 35, Appl	244	6	1.7	174	2		
172	6	1.7	21	US-08-388-883B-35	Sequence 35, Appl	245	6	1.7	174	2		
173	6	1.7	21	US-08-462-211A-35	Sequence 35, Appl	246	6	1.7	174	2		

247	6	1.7	174	2	US-08-683-262B-50	Sequence 50, Appl	320	6	1.7	307	4	US-09-368-402-3	Sequence 3, Appl
248	6	1.7	174	2	US-08-683-262B-51	Sequence 51, Appl	321	6	1.7	314	1	US-08-040-753-2	Sequence 2, Appl
249	6	1.7	174	2	US-08-683-262B-52	Sequence 52, Appl	322	6	1.7	314	4	US-09-004-838-14	Sequence 14, Appl
250	6	1.7	174	2	US-08-683-262B-53	Sequence 53, Appl	323	6	1.7	315	4	US-09-720-817-3	Sequence 3, Appl
251	6	1.7	174	2	US-08-683-262B-54	Sequence 54, Appl	324	6	1.7	315	4	US-09-720-817-6	Sequence 6, Appl
252	6	1.7	174	2	US-08-683-262B-55	Sequence 55, Appl	325	6	1.7	316	2	US-08-842-842-7	Sequence 7, Appl
253	6	1.7	174	2	US-08-683-262B-56	Sequence 56, Appl	326	6	1.7	316	4	US-08-989-362-2	Sequence 2, Appl
254	6	1.7	174	2	US-08-683-262B-57	Sequence 57, Appl	327	6	1.7	316	4	US-09-052-521C-2	Sequence 2, Appl
255	6	1.7	174	2	US-08-683-262B-62	Sequence 62, Appl	328	6	1.7	319	4	US-08-983-035A-42	Sequence 42, Appl
256	6	1.7	174	3	US-08-480-173A-44	Sequence 44, Appl	329	6	1.7	327	4	US-09-134-001C-3471	Sequence 3471, Ap
257	6	1.7	174	3	US-08-480-173A-45	Sequence 45, Appl	330	6	1.7	330	1	US-08-118-270-19	Sequence 19, Appl
258	6	1.7	174	3	US-08-480-173A-48	Sequence 48, Appl	331	6	1.7	330	5	PCT-US93-08528-19	Sequence 19, Appl
259	6	1.7	174	3	US-08-484-408A-44	Sequence 44, Appl	332	6	1.7	331	2	US-08-997-080-182	Sequence 182, App
260	6	1.7	174	3	US-08-484-408A-45	Sequence 45, Appl	333	6	1.7	331	2	US-08-997-362-182	Sequence 182, App
261	6	1.7	174	3	US-08-484-408A-48	Sequence 48, Appl	334	6	1.7	331	4	US-09-095-855-182	Sequence 182, App
262	6	1.7	174	4	US-09-361-707-42	Sequence 42, Appl	335	6	1.7	331	4	US-09-324-542-182	Sequence 182, App
263	6	1.7	174	4	US-09-361-707-43	Sequence 43, Appl	336	6	1.7	331	4	US-09-205-426-182	Sequence 182, App
264	6	1.7	174	4	US-09-361-707-45	Sequence 45, Appl	337	6	1.7	335	4	US-08-983-035A-44	Sequence 44, Appl
265	6	1.7	174	4	US-09-361-707-46	Sequence 46, Appl	338	6	1.7	336	3	US-09-095-153-2	Sequence 2, Appl
266	6	1.7	174	4	US-09-361-707-47	Sequence 47, Appl	339	6	1.7	340	2	US-08-446-875-16	Sequence 16, Appl
267	6	1.7	174	4	US-09-361-707-48	Sequence 48, Appl	340	6	1.7	342	1	US-08-096-182A-4	Sequence 4, Appl
268	6	1.7	174	4	US-09-361-707-50	Sequence 50, Appl	341	6	1.7	342	1	US-08-877-109-4	Sequence 4, Appl
269	6	1.7	174	4	US-09-361-707-51	Sequence 51, Appl	342	6	1.7	342	3	US-08-798-760-4	Sequence 4, Appl
270	6	1.7	174	4	US-09-361-707-52	Sequence 52, Appl	343	6	1.7	342	5	PCT-US94-08327-4	Sequence 4, Appl
271	6	1.7	174	4	US-09-361-707-53	Sequence 53, Appl	344	6	1.7	343	2	US-08-446-875-2	Sequence 2, Appl
272	6	1.7	174	4	US-09-361-707-54	Sequence 54, Appl	345	6	1.7	343	2	US-08-102-385G-2	Sequence 2, Appl
273	6	1.7	174	4	US-09-361-707-55	Sequence 55, Appl	346	6	1.7	347	4	US-09-039-046-2	Sequence 2, Appl
274	6	1.7	174	4	US-09-361-707-56	Sequence 56, Appl	347	6	1.7	350	4	US-09-161-241-9	Sequence 9, Appl
275	6	1.7	174	4	US-09-361-707-57	Sequence 57, Appl	348	6	1.7	353	4	US-08-983-035A-40	Sequence 40, Appl
276	6	1.7	174	4	US-09-361-707-62	Sequence 62, Appl	349	6	1.7	360	2	US-08-319-866-2	Sequence 2, Appl
277	6	1.7	174	6	5204096-1	Patent No. 5204096	350	6	1.7	361	4	US-09-134-001C-3862	Sequence 3862, Ap
278	6	1.7	174	6	5204096-2	Patent No. 5204096	351	6	1.7	362	4	US-09-485-648-6	Sequence 6, Appl
279	6	1.7	174	6	5204096-5	Patent No. 5204096	352	6	1.7	362	4	US-09-503-565-6	Sequence 6, Appl
280	6	1.7	174	6	5198542-6	Patent No. 5198542	353	6	1.7	362	4	US-09-485-649-9	Sequence 6, Appl
281	6	1.7	175	6	5198542-6	Patent No. 5198542	354	6	1.7	363	1	US-08-096-182A-6	Sequence 6, Appl
282	6	1.7	182	4	US-09-134-001C-2842	Sequence 2842, Ap	355	6	1.7	363	1	US-08-877-109-6	Sequence 6, Appl
283	6	1.7	189	4	US-09-134-001C-3795	Sequence 3795, Ap	356	6	1.7	363	2	US-08-697-221-17	Sequence 17, Appl
284	6	1.7	191	3	US-08-928-361B-26	Sequence 26, Appl	357	6	1.7	363	2	US-08-697-221-18	Sequence 18, Appl
285	6	1.7	194	4	US-09-171-517B-8	Sequence 8, Appl	358	6	1.7	363	2	US-08-697-221-19	Sequence 19, Appl
286	6	1.7	197	4	US-09-112-248-2	Sequence 2, Appl	359	6	1.7	363	2	US-08-697-221-20	Sequence 20, Appl
287	6	1.7	218	1	US-08-463-115-92	Sequence 92, Appl	360	6	1.7	363	2	US-08-697-221-21	Sequence 21, Appl
288	6	1.7	218	1	US-08-465-388-52	Sequence 92, Appl	361	6	1.7	363	2	US-08-697-221-22	Sequence 22, Appl
289	6	1.7	219	1	US-08-463-115-91	Sequence 91, Appl	362	6	1.7	363	2	US-08-697-221-23	Sequence 23, Appl
290	6	1.7	219	1	US-08-465-388-91	Sequence 91, Appl	363	6	1.7	363	2	US-08-697-221-24	Sequence 24, Appl
291	6	1.7	223	4	US-09-171-461-11	Sequence 11, Appl	364	6	1.7	363	3	US-08-798-760-6	Sequence 6, Appl
292	6	1.7	233	1	US-08-607-269-23	Sequence 23, Appl	365	6	1.7	363	4	US-08-983-035A-26	Sequence 26, Appl
293	6	1.7	233	5	PCT-US95-04600-23	Sequence 23, Appl	366	6	1.7	363	5	PCT-US94-08327-6	Sequence 6, Appl
294	6	1.7	234	4	US-08-936-165A-517	Sequence 517, App	367	6	1.7	371	4	US-09-134-001C-4502	Sequence 4502, Ap
295	6	1.7	236	1	US-08-315-695-18	Sequence 18, Appl	368	6	1.7	371	4	US-09-814-951A-2	Sequence 2, Appl
296	6	1.7	241	4	US-08-823-120-1	Sequence 1, Appl	369	6	1.7	374	4	US-08-983-035A-28	Sequence 28, Ap
297	6	1.7	245	3	US-09-286-690-2	Sequence 2, Appl	370	6	1.7	374	4	US-09-134-001C-2939	Sequence 2939, Ap
298	6	1.7	251	1	US-08-209-747-8	Sequence 8, Appl	371	6	1.7	381	4	US-08-983-035A-36	Sequence 36, Appl
299	6	1.7	251	1	US-08-458-298-8	Sequence 8, Appl	372	6	1.7	382	2	US-08-504-265B-75	Sequence 75, Appl
300	6	1.7	253	4	US-08-983-035A-30	Sequence 30, Appl	373	6	1.7	382	4	US-09-413-814-12	Sequence 12, Appl
301	6	1.7	254	2	US-08-948-616-9	Sequence 9, Appl	374	6	1.7	386	1	US-09-331-924-9	Sequence 9, Appl
302	6	1.7	254	2	US-09-193-510-9	Sequence 9, Appl	375	6	1.7	389	1	US-08-105-483-216	Sequence 216, App
303	6	1.7	254	4	US-09-368-402-9	Sequence 9, Appl	376	6	1.7	389	1	US-08-105-483-219	Sequence 219, App
304	6	1.7	261	4	US-09-414-436-3	Sequence 3, Appl	377	6	1.7	389	1	US-08-709-209-216	Sequence 216, App
305	6	1.7	263	1	US-08-117-083-9	Sequence 9, Appl	378	6	1.7	389	1	US-08-709-209-219	Sequence 219, App
306	6	1.7	270	4	US-08-983-035A-32	Sequence 32, Appl	379	6	1.7	389	1	US-08-458-101-216	Sequence 216, App
307	6	1.7	280	4	US-09-720-817-1	Sequence 1, Appl	380	6	1.7	389	1	US-08-458-101-219	Sequence 219, App
308	6	1.7	294	3	US-08-996-139-11	Sequence 11, Appl	381	6	1.7	389	3	US-08-486-099-106	Sequence 106, App
309	6	1.7	294	4	US-08-995-659-11	Sequence 11, Appl	382	6	1.7	389	3	US-08-360-107A-116	Sequence 116, App
310	6	1.7	294	4	US-09-215-649A-11	Sequence 11, Appl	383	6	1.7	389	3	US-08-484-223B-106	Sequence 106, App
311	6	1.7	294	4	US-09-517-780-11	Sequence 11, Appl	384	6	1.7	389	3	US-09-919-597-106	Sequence 106, App
312	6	1.7	299	4	US-09-069-023-20	Sequence 20, Appl	385	6	1.7	389	3	US-08-475-668A-106	Sequence 106, App
313	6	1.7	300	3	US-08-765-856-2	Sequence 2, Appl	386	6	1.7	389	3	US-08-485-551A-106	Sequence 106, App
314	6	1.7	300	3	US-08-935-009A-2	Sequence 2, Appl	387	6	1.7	389	3	US-08-471-913A-106	Sequence 106, App
315	6	1.7	302	3	US-08-765-856-4	Sequence 4, Appl	388	6	1.7	389	4	US-08-485-264A-106	Sequence 106, App
316	6	1.7	302	4	US-08-935-009A-4	Sequence 4, Appl	389	6	1.7	389	4	US-08-474-349A-106	Sequence 106, App
317	6	1.7	303	3	US-08-928-361B-7	Sequence 7, Appl	390	6	1.7	390	1	US-08-347-792-15	Sequence 15, Appl
318	6	1.7	307	2	US-08-948-616-3	Sequence 3, Appl	391	6	1.7	390	1	US-08-431-357-15	Sequence 15, Appl
319	6	1.7	307	2	US-09-193-510-3	Sequence 3, Appl	392	6	1.7	390	4	US-08-392-542-3	Sequence 3, Appl

393	6	1.7	390	4	US-08-894-327-3	Sequence 3, Appl1	466	6	1.7	410	4	US-09-650-855-41	Sequence 41, Appl1
394	6	1.7	390	4	US-09-685-027-3	Sequence 3, Appl1	467	6	1.7	412	4	US-09-445-472-1	Sequence 12, Appl1
395	6	1.7	390	5	PCT-US95-15353-15	Sequence 15, Appl1	468	6	1.7	413	2	US-08-759-593-11	Sequence 12, Appl1
396	6	1.7	393	1	US-08-047-041A-25	Sequence 25, Appl1	469	6	1.7	413	2	US-08-759-593-11	Sequence 12, Appl1
397	6	1.7	393	1	US-08-047-041A-26	Sequence 26, Appl1	470	6	1.7	414	1	US-08-255-471-9	Sequence 9, Appl1
398	6	1.7	393	1	US-08-047-041A-27	Sequence 27, Appl1	471	6	1.7	428	4	US-08-403-797-2	Sequence 2, Appl1
399	6	1.7	393	1	US-08-047-041A-28	Sequence 28, Appl1	472	6	1.7	428	4	US-08-883-515-2	Sequence 2, Appl1
400	6	1.7	393	1	US-08-347-792-2	Sequence 2, Appl1	473	6	1.7	433	3	US-08-443-644-23	Sequence 23, Appl1
401	6	1.7	393	1	US-08-390-516C-6	Sequence 6, Appl1	474	6	1.7	434	3	US-08-444-644-31	Sequence 31, Appl1
402	6	1.7	393	1	US-08-390-516C-7	Sequence 7, Appl1	475	6	1.7	434	3	US-08-444-644-40	Sequence 40, Appl1
403	6	1.7	393	1	US-08-390-516C-8	Sequence 8, Appl1	476	6	1.7	434	3	US-08-444-644-46	Sequence 46, Appl1
404	6	1.7	393	1	US-08-390-516C-9	Sequence 9, Appl1	477	6	1.7	434	3	US-08-232-246A-23	Sequence 23, Appl1
405	6	1.7	393	1	US-08-431-357-2	Sequence 2, Appl1	478	6	1.7	434	4	US-08-232-246A-31	Sequence 31, Appl1
406	6	1.7	393	1	US-08-390-515A-6	Sequence 6, Appl1	479	6	1.7	434	4	US-08-232-246A-40	Sequence 40, Appl1
407	6	1.7	393	1	US-08-390-515A-7	Sequence 7, Appl1	480	6	1.7	434	4	US-08-232-246A-46	Sequence 46, Appl1
408	6	1.7	393	1	US-08-390-515A-8	Sequence 8, Appl1	481	6	1.7	437	1	US-08-135-119-2	Sequence 2, Appl1
409	6	1.7	393	1	US-08-795-006A-9	Sequence 9, Appl1	482	6	1.7	437	2	US-08-481-814A-7	Sequence 7, Appl1
410	6	1.7	393	2	US-08-697-221-2	Sequence 32, Appl1	483	6	1.7	439	2	US-08-959-638-9	Sequence 9, Appl1
411	6	1.7	393	2	US-08-697-221-3	Sequence 3, Appl1	484	6	1.7	446	4	US-09-457-046B-74	Sequence 74, Appl1
412	6	1.7	393	2	US-08-697-221-4	Sequence 4, Appl1	485	6	1.7	456	1	US-08-624-125-20	Sequence 20, Appl1
413	6	1.7	393	2	US-08-697-221-5	Sequence 5, Appl1	486	6	1.7	460	1	US-08-342-411A-2	Sequence 2, Appl1
414	6	1.7	393	2	US-08-697-221-6	Sequence 6, Appl1	487	6	1.7	461	1	US-08-194-338-4	Sequence 4, Appl1
415	6	1.7	393	2	US-08-697-221-7	Sequence 7, Appl1	488	6	1.7	461	1	US-08-330-518-2	Sequence 2, Appl1
416	6	1.7	393	2	US-08-697-221-8	Sequence 8, Appl1	489	6	1.7	461	1	US-08-330-518-2	Sequence 2, Appl1
417	6	1.7	393	2	US-08-697-221-9	Sequence 9, Appl1	490	6	1.7	461	2	US-08-646-248-2	Sequence 2, Appl1
418	6	1.7	393	2	US-08-697-221-10	Sequence 10, Appl1	491	6	1.7	461	2	PCT-US95-13924-2	Sequence 2, Appl1
419	6	1.7	393	2	US-08-697-221-11	Sequence 11, Appl1	492	6	1.7	461	5	PCT-US95-13931-2	Sequence 2, Appl1
420	6	1.7	393	2	US-08-697-221-12	Sequence 12, Appl1	493	6	1.7	468	2	US-08-839-008-7	Sequence 7, Appl1
421	6	1.7	393	2	US-08-697-221-13	Sequence 13, Appl1	494	6	1.7	468	4	US-09-032-523-8	Sequence 8, Appl1
422	6	1.7	393	2	US-08-697-221-14	Sequence 14, Appl1	495	6	1.7	476	4	US-09-134-001C-4458	Sequence 4458, Ap
423	6	1.7	393	2	US-08-697-221-15	Sequence 15, Appl1	496	6	1.7	484	3	US-09-263-023-4	Sequence 4, Appl1
424	6	1.7	393	2	US-08-697-221-16	Sequence 16, Appl1	497	6	1.7	484	4	US-08-471-867-4	Sequence 4, Appl1
425	6	1.7	393	2	US-08-801-718-7	Sequence 7, Appl1	498	6	1.7	486	4	US-08-906-743-4	Sequence 4, Appl1
426	6	1.7	393	2	US-08-801-718-8	Sequence 8, Appl1	499	6	1.7	488	1	US-07-794-393-2	Sequence 2, Appl1
427	6	1.7	393	2	US-08-801-718-9	Sequence 9, Appl1	500	6	1.7	488	1	US-08-001-711-2	Sequence 2, Appl1
428	6	1.7	393	2	US-08-247-904B-12	Sequence 12, Appl1	501	6	1.7	488	3	US-09-165-042-1	Sequence 1, Appl1
429	6	1.7	393	2	US-08-675-631-1	Sequence 1, Appl1	502	6	1.7	488	4	US-08-704-711A-22	Sequence 22, Appl1
430	6	1.7	393	3	US-08-767-942A-23	Sequence 23, Appl1	503	6	1.7	488	4	US-09-521-220-22	Sequence 22, Appl1
431	6	1.7	393	4	US-08-392-542-2	Sequence 32, Appl1	504	6	1.7	488	4	US-09-391-104-31	Sequence 31, Appl1
432	6	1.7	393	4	US-09-184-073-32	Sequence 32, Appl1	505	6	1.7	489	4	US-08-448-489-11	Sequence 11, Appl1
433	6	1.7	393	4	US-08-328-673A-9	Sequence 9, Appl1	506	6	1.7	495	3	US-09-079-415-4	Sequence 4, Appl1
434	6	1.7	393	4	US-08-894-327-2	Sequence 2, Appl1	507	6	1.7	498	1	US-08-080-855-1	Sequence 1, Appl1
435	6	1.7	393	4	US-09-308-914-2	Sequence 2, Appl1	508	6	1.7	500	4	US-09-326-203A-17	Sequence 17, Appl1
436	6	1.7	393	4	US-09-308-914-3	Sequence 3, Appl1	509	6	1.7	505	1	US-08-221-750A-5	Sequence 5, Appl1
437	6	1.7	393	4	US-09-305-914-4	Sequence 4, Appl1	510	6	1.7	507	5	PCT-US93-08386-8	Sequence 8, Appl1
438	6	1.7	393	4	US-09-685-027-2	Sequence 2, Appl1	511	6	1.7	522	4	US-08-894-818B-3	Sequence 3, Appl1
439	6	1.7	393	4	US-09-417-278A-2	Sequence 2, Appl1	512	6	1.7	522	4	US-09-445-472-4	Sequence 4, Appl1
440	6	1.7	393	4	US-09-331-924-8	Sequence 8, Appl1	513	6	1.7	527	2	US-08-365-486A-26	Sequence 26, Appl1
441	6	1.7	393	5	PCT-US95-15353-2	Sequence 2, Appl1	514	6	1.7	527	4	US-09-126-109-10	Sequence 10, Appl1
442	6	1.7	394	4	US-08-134-001C-4834	Sequence 4834, Ap	515	6	1.7	527	4	US-08-880-342-26	Sequence 26, Appl1
443	6	1.7	394	4	US-09-081-975-4	Sequence 4, Appl1	516	6	1.7	527	4	US-08-583-035A-38	Sequence 38, Appl1
444	6	1.7	396	2	US-09-061-337-12	Sequence 12, Appl1	517	6	1.7	535	4	US-08-458-261B-2	Sequence 2, Appl1
445	6	1.7	396	2	US-09-122-129-12	Sequence 12, Appl1	518	6	1.7	538	1	US-08-456-837-2	Sequence 2, Appl1
446	6	1.7	396	3	US-09-340-991-12	Sequence 12, Appl1	519	6	1.7	538	1	US-08-457-342-2	Sequence 2, Appl1
447	6	1.7	396	4	US-08-974-609-12	Sequence 12, Appl1	520	6	1.7	538	1	US-08-457-646A-2	Sequence 2, Appl1
448	6	1.7	396	4	US-09-242-859A-2	Sequence 2, Appl1	521	6	1.7	538	1	US-08-458-076A-2	Sequence 2, Appl1
449	6	1.7	396	4	US-08-242-859A-6	Sequence 6, Appl1	522	6	1.7	538	2	US-08-457-335A-2	Sequence 2, Appl1
450	6	1.7	396	4	US-08-549-098-12	Sequence 12, Appl1	523	6	1.7	538	2	US-08-729-214-24	Sequence 24, Appl1
451	6	1.7	398	1	US-08-471-791-20	Sequence 20, Appl1	524	6	1.7	538	3	US-09-028-934-24	Sequence 24, Appl1
452	6	1.7	398	4	US-08-926-522-6	Sequence 6, Appl1	525	6	1.7	538	3	US-09-028-934-24	Sequence 24, Appl1
453	6	1.7	398	5	PCT-US91-01746-20	Sequence 20, Appl1	526	6	1.7	539	4	US-09-036-987A-11	Sequence 11, Appl1
454	6	1.7	401	2	US-08-839-008-5	Sequence 5, Appl1	527	6	1.7	539	4	US-09-370-700-11	Sequence 11, Appl1
455	6	1.7	401	4	US-08-983-035A-34	Sequence 34, Appl1	528	6	1.7	546	2	US-08-713-928B-4	Sequence 4, Appl1
456	6	1.7	402	2	US-09-347-801-16	Sequence 16, Appl1	529	6	1.7	552	4	US-08-557-006C-40	Sequence 40, Appl1
457	6	1.7	403	2	US-09-061-337-10	Sequence 10, Appl1	530	6	1.7	552	4	US-07-862-588B-4	Sequence 2, Appl1
458	6	1.7	403	3	US-09-122-129-10	Sequence 10, Appl1	531	6	1.7	553	4	US-08-906-743-2	Sequence 2, Appl1
459	6	1.7	403	3	US-09-340-991-10	Sequence 10, Appl1	532	6	1.7	556	2	US-07-862-588B-4	Sequence 4, Appl1
460	6	1.7	403	4	US-08-974-609-10	Sequence 10, Appl1	533	6	1.7	575	3	US-08-948-564-16	Sequence 16, Appl1
461	6	1.7	403	4	US-09-549-098-10	Sequence 10, Appl1	534	6	1.7	577	1	US-08-183-266A-49	Sequence 49, Appl1
462	6	1.7	408	1	US-08-127-278-4	Sequence 4, Appl1	535	6	1.7	587	1	US-08-398-008A-2	Sequence 2, Appl1
463	6	1.7	408	1	US-08-555-860-4	Sequence 4, Appl1	536	6	1.7	587	2	US-08-893-333-2	Sequence 2, Appl1
464	6	1.7	408	4	US-09-814-951A-4	Sequence 4, Appl1	537	6	1.7	605	4	US-09-105-058C-24	Sequence 24, Appl1
465	6	1.7	410	4	US-09-651-656-41	Sequence 41, Appl1	538	6	1.7	608	4	US-09-134-001C-3855	Sequence 3855, Ap

539	6	1.7	610	2	US-08-724-394A-5	Sequence 5, Appl1	612	6	1.7	652	3	US-08-996-441B-98	Sequence 98, Appl1
540	6	1.7	619	1	US-08-465-746-2	Sequence 2, Appl1	613	6	1.7	652	3	US-08-996-441B-108	Sequence 108, App
541	6	1.7	619	1	US-08-214-164-2	Sequence 2, Appl1	614	6	1.7	652	3	US-08-996-441B-110	Sequence 110, App
542	6	1.7	619	2	US-08-467-852A-3	Sequence 3, Appl1	615	6	1.7	652	3	US-08-996-441B-111	Sequence 111, App
543	6	1.7	619	2	US-08-246-636-2	Sequence 2, Appl1	616	6	1.7	652	3	US-08-996-441B-113	Sequence 113, App
544	6	1.7	619	2	US-08-247-491A-3	Sequence 3, Appl1	617	6	1.7	652	3	US-08-993-722A-2	Sequence 2, Appl1
545	6	1.7	619	2	US-08-319-795-2	Sequence 2, Appl1	618	6	1.7	652	3	US-08-993-722A-4	Sequence 4, Appl1
546	6	1.7	619	2	US-08-468-985-2	Sequence 2, Appl1	619	6	1.7	652	3	US-08-993-722A-6	Sequence 6, Appl1
547	6	1.7	619	3	US-08-312-949-2	Sequence 2, Appl1	620	6	1.7	652	3	US-08-993-722A-8	Sequence 8, Appl1
548	6	1.7	620	4	US-08-982-785A-10	Sequence 10, Appl1	621	6	1.7	652	3	US-08-993-722A-10	Sequence 10, Appl1
549	6	1.7	627	4	US-09-071-035-452	Sequence 452, App	622	6	1.7	652	3	US-08-993-722A-12	Sequence 12, Appl1
550	6	1.7	641	4	US-08-811-481-2	Sequence 2, Appl1	623	6	1.7	652	3	US-08-993-722A-14	Sequence 14, Appl1
551	6	1.7	644	1	US-07-828-788A-4	Sequence 4, Appl1	624	6	1.7	652	3	US-08-993-722A-16	Sequence 16, Appl1
552	6	1.7	644	1	US-08-072-281-2	Sequence 2, Appl1	625	6	1.7	652	3	US-08-993-722A-18	Sequence 18, Appl1
553	6	1.7	644	1	US-08-295-060-2	Sequence 2, Appl1	626	6	1.7	652	3	US-08-993-722A-20	Sequence 20, Appl1
554	6	1.7	644	1	US-08-759-446-2	Sequence 2, Appl1	627	6	1.7	652	3	US-08-993-722A-22	Sequence 22, Appl1
555	6	1.7	644	1	US-09-027-998A-2	Sequence 2, Appl1	628	6	1.7	652	3	US-08-993-722A-24	Sequence 24, Appl1
556	6	1.7	644	5	PCR-US92-11337-4	Sequence 4, Appl1	629	6	1.7	652	3	US-08-993-722A-26	Sequence 26, Appl1
557	6	1.7	645	1	US-08-295-060-4	Sequence 2, Appl1	630	6	1.7	652	3	US-08-993-722A-28	Sequence 28, Appl1
558	6	1.7	648	1	US-08-072-070-2	Sequence 2, Appl1	631	6	1.7	652	3	US-08-993-722A-30	Sequence 30, Appl1
559	6	1.7	648	1	US-08-469-434-2	Sequence 2, Appl1	632	6	1.7	652	3	US-08-993-722A-32	Sequence 32, Appl1
560	6	1.7	648	1	US-08-214-222-2	Sequence 2, Appl1	633	6	1.7	652	3	US-08-993-722A-34	Sequence 34, Appl1
561	6	1.7	648	1	US-08-467-852A-2	Sequence 2, Appl1	634	6	1.7	652	3	US-08-993-722A-36	Sequence 36, Appl1
562	6	1.7	648	2	US-08-468-718-2	Sequence 2, Appl1	635	6	1.7	652	3	US-08-993-722A-38	Sequence 38, Appl1
563	6	1.7	648	2	US-08-247-491A-2	Sequence 2, Appl1	636	6	1.7	652	3	US-08-993-722A-40	Sequence 40, Appl1
564	6	1.7	648	3	US-08-446-201-3	Sequence 3, Appl1	637	6	1.7	652	3	US-08-993-722A-42	Sequence 42, Appl1
565	6	1.7	649	3	US-08-996-441B-109	Sequence 109, App	638	6	1.7	652	3	US-08-993-722A-44	Sequence 44, Appl1
566	6	1.7	649	3	US-08-993-722A-109	Sequence 109, App	639	6	1.7	652	3	US-08-993-722A-46	Sequence 46, Appl1
567	6	1.7	649	3	US-08-993-170A-109	Sequence 109, App	640	6	1.7	652	3	US-08-993-722A-48	Sequence 48, Appl1
568	6	1.7	649	3	US-08-993-775B-109	Sequence 109, App	641	6	1.7	652	3	US-08-993-722A-50	Sequence 50, Appl1
569	6	1.7	651	3	US-08-996-441B-52	Sequence 52, Appl1	642	6	1.7	652	3	US-08-993-722A-54	Sequence 54, Appl1
570	6	1.7	651	3	US-08-996-441B-56	Sequence 56, Appl1	643	6	1.7	652	3	US-08-993-722A-60	Sequence 60, Appl1
571	6	1.7	651	3	US-08-996-441B-58	Sequence 58, Appl1	644	6	1.7	652	3	US-08-993-722A-64	Sequence 64, Appl1
572	6	1.7	651	3	US-08-993-722A-52	Sequence 52, Appl1	645	6	1.7	652	3	US-08-993-722A-66	Sequence 66, Appl1
573	6	1.7	651	3	US-08-993-722A-56	Sequence 56, Appl1	646	6	1.7	652	3	US-08-993-722A-68	Sequence 68, Appl1
574	6	1.7	651	3	US-08-993-170A-58	Sequence 58, Appl1	647	6	1.7	652	3	US-08-993-722A-98	Sequence 98, Appl1
575	6	1.7	651	3	US-08-993-170A-52	Sequence 52, Appl1	648	6	1.7	652	3	US-08-993-722A-108	Sequence 108, App
576	6	1.7	651	3	US-08-993-170A-56	Sequence 56, Appl1	649	6	1.7	652	3	US-08-993-722A-110	Sequence 110, App
577	6	1.7	651	3	US-08-993-170A-58	Sequence 58, Appl1	650	6	1.7	652	3	US-08-993-722A-111	Sequence 111, App
578	6	1.7	651	3	US-08-993-775B-52	Sequence 52, Appl1	651	6	1.7	652	3	US-08-993-722A-113	Sequence 113, App
579	6	1.7	651	3	US-08-993-775B-58	Sequence 58, Appl1	652	6	1.7	652	3	US-08-993-170A-2	Sequence 2, Appl1
580	6	1.7	651	3	US-08-993-775B-58	Sequence 58, Appl1	653	6	1.7	652	3	US-08-993-170A-4	Sequence 4, Appl1
581	6	1.7	652	3	US-08-996-441B-2	Sequence 2, Appl1	654	6	1.7	652	3	US-08-993-170A-6	Sequence 6, Appl1
582	6	1.7	652	3	US-08-996-441B-6	Sequence 6, Appl1	655	6	1.7	652	3	US-08-993-170A-8	Sequence 8, Appl1
583	6	1.7	652	3	US-08-996-441B-8	Sequence 8, Appl1	656	6	1.7	652	3	US-08-993-170A-10	Sequence 10, Appl1
584	6	1.7	652	3	US-08-996-441B-10	Sequence 10, Appl1	657	6	1.7	652	3	US-08-993-170A-12	Sequence 12, Appl1
585	6	1.7	652	3	US-08-996-441B-12	Sequence 12, Appl1	658	6	1.7	652	3	US-08-993-170A-14	Sequence 14, Appl1
586	6	1.7	652	3	US-08-996-441B-14	Sequence 14, Appl1	659	6	1.7	652	3	US-08-993-170A-16	Sequence 16, Appl1
587	6	1.7	652	3	US-08-996-441B-16	Sequence 16, Appl1	660	6	1.7	652	3	US-08-993-170A-18	Sequence 18, Appl1
588	6	1.7	652	3	US-08-996-441B-18	Sequence 18, Appl1	661	6	1.7	652	3	US-08-993-170A-20	Sequence 20, Appl1
589	6	1.7	652	3	US-08-996-441B-20	Sequence 20, Appl1	662	6	1.7	652	3	US-08-993-170A-22	Sequence 22, Appl1
590	6	1.7	652	3	US-08-996-441B-22	Sequence 22, Appl1	663	6	1.7	652	3	US-08-993-170A-24	Sequence 24, Appl1
591	6	1.7	652	3	US-08-996-441B-24	Sequence 24, Appl1	664	6	1.7	652	3	US-08-993-170A-26	Sequence 26, Appl1
592	6	1.7	652	3	US-08-996-441B-26	Sequence 26, Appl1	665	6	1.7	652	3	US-08-993-170A-28	Sequence 28, Appl1
593	6	1.7	652	3	US-08-996-441B-28	Sequence 28, Appl1	666	6	1.7	652	3	US-08-993-170A-30	Sequence 30, Appl1
594	6	1.7	652	3	US-08-996-441B-30	Sequence 30, Appl1	667	6	1.7	652	3	US-08-993-170A-32	Sequence 32, Appl1
595	6	1.7	652	3	US-08-996-441B-32	Sequence 32, Appl1	668	6	1.7	652	3	US-08-993-170A-34	Sequence 34, Appl1
596	6	1.7	652	3	US-08-996-441B-34	Sequence 34, Appl1	669	6	1.7	652	3	US-08-993-170A-36	Sequence 36, Appl1
597	6	1.7	652	3	US-08-996-441B-36	Sequence 36, Appl1	670	6	1.7	652	3	US-08-993-170A-38	Sequence 38, Appl1
598	6	1.7	652	3	US-08-996-441B-38	Sequence 38, Appl1	671	6	1.7	652	3	US-08-993-170A-40	Sequence 40, Appl1
599	6	1.7	652	3	US-08-996-441B-40	Sequence 40, Appl1	672	6	1.7	652	3	US-08-993-170A-42	Sequence 42, Appl1
600	6	1.7	652	3	US-08-996-441B-42	Sequence 42, Appl1	673	6	1.7	652	3	US-08-993-170A-44	Sequence 44, Appl1
601	6	1.7	652	3	US-08-996-441B-44	Sequence 44, Appl1	674	6	1.7	652	3	US-08-993-170A-46	Sequence 46, Appl1
602	6	1.7	652	3	US-08-996-441B-46	Sequence 46, Appl1	675	6	1.7	652	3	US-08-993-170A-48	Sequence 48, Appl1
603	6	1.7	652	3	US-08-996-441B-48	Sequence 48, Appl1	676	6	1.7	652	3	US-08-993-170A-50	Sequence 50, Appl1
604	6	1.7	652	3	US-08-996-441B-50	Sequence 50, Appl1	677	6	1.7	652	3	US-08-993-170A-54	Sequence 54, Appl1
605	6	1.7	652	3	US-08-996-441B-54	Sequence 54, Appl1	678	6	1.7	652	3	US-08-993-170A-60	Sequence 60, Appl1
606	6	1.7	652	3	US-08-996-441B-60	Sequence 60, Appl1	679	6	1.7	652	3	US-08-993-170A-62	Sequence 62, Appl1
607	6	1.7	652	3	US-08-996-441B-62	Sequence 62, Appl1	680	6	1.7	652	3	US-08-993-170A-64	Sequence 64, Appl1
608	6	1.7	652	3	US-08-996-441B-64	Sequence 64, Appl1	681	6	1.7	652	3	US-08-993-170A-66	Sequence 66, Appl1
609	6	1.7	652	3	US-08-996-441B-66	Sequence 66, Appl1	682	6	1.7	652	3	US-08-993-170A-68	Sequence 68, Appl1
610	6	1.7	652	3	US-08-996-441B-68	Sequence 68, Appl1	683	6	1.7	652	3	US-08-993-170A-98	Sequence 98, Appl1
611	6	1.7	652	3	US-08-996-441B-98	Sequence 98, Appl1	684	6	1.7	652	3		

685	6	1.7	652	3	US-08-993-170A-108	Sequence 108, App	758	6	1.7	803	2	US-08-611-928-10	Sequence 10, Appl
686	6	1.7	652	3	US-08-993-170A-110	Sequence 110, App	759	6	1.7	803	3	US-09-173-891-10	Sequence 10, Appl
687	6	1.7	652	3	US-08-993-170A-111	Sequence 111, App	760	6	1.7	803	4	US-09-076-137-12	Sequence 12, Appl
688	6	1.7	652	3	US-08-993-170A-113	Sequence 113, App	761	6	1.7	803	5	PCT-US92-03624-12	Sequence 12, Appl
689	6	1.7	652	3	US-08-993-775B-2	Sequence 2, Appl	762	6	1.7	808	1	US-08-471-251A-2	Sequence 2, Appl
690	6	1.7	652	3	US-08-993-775B-4	Sequence 4, Appl	763	6	1.7	811	4	US-09-199-637A-93	Sequence 93, Appl
691	6	1.7	652	3	US-08-993-775B-6	Sequence 6, Appl	764	6	1.7	873	2	US-08-912-129A-61	Sequence 61, Appl
692	6	1.7	652	3	US-08-993-775B-8	Sequence 8, Appl	765	6	1.7	961	5	PCT-US93-11725-4	Sequence 4, Appl
693	6	1.7	652	3	US-08-993-775B-10	Sequence 10, Appl	766	6	1.7	964	3	US-08-860-339-18	Sequence 18, Appl
694	6	1.7	652	3	US-08-993-775B-12	Sequence 12, Appl	767	6	1.7	964	4	US-09-403-618A-6	Sequence 6, Appl
695	6	1.7	652	3	US-08-993-775B-14	Sequence 14, Appl	768	6	1.7	1012	4	US-08-811-481-16	Sequence 16, Appl
696	6	1.7	652	3	US-08-993-775B-16	Sequence 16, Appl	769	6	1.7	1030	4	US-09-091-117-2	Sequence 2, Appl
697	6	1.7	652	3	US-08-993-775B-18	Sequence 18, Appl	770	6	1.7	1048	4	US-09-171-699-10	Sequence 10, Appl
698	6	1.7	652	3	US-08-993-775B-20	Sequence 20, Appl	771	6	1.7	1070	3	US-08-922-635-22	Sequence 22, Appl
699	6	1.7	652	3	US-08-993-775B-22	Sequence 22, Appl	772	6	1.7	1084	4	US-09-221-725B-3	Sequence 3, Appl
700	6	1.7	652	3	US-08-993-775B-24	Sequence 24, Appl	773	6	1.7	1147	1	US-08-131-365B-38	Sequence 38, Appl
701	6	1.7	652	3	US-08-993-775B-26	Sequence 26, Appl	774	6	1.7	1147	2	US-08-668-123-38	Sequence 38, Appl
702	6	1.7	652	3	US-08-993-775B-28	Sequence 28, Appl	775	6	1.7	1169	1	US-08-315-468-4	Sequence 4, Appl
703	6	1.7	652	3	US-08-993-775B-30	Sequence 30, Appl	776	6	1.7	1196	4	US-08-881-706-2	Sequence 2, Appl
704	6	1.7	652	3	US-08-993-775B-32	Sequence 32, Appl	777	6	1.7	1211	4	US-09-134-001C-4820	Sequence 4820, Ap
705	6	1.7	652	3	US-08-993-775B-34	Sequence 34, Appl	778	6	1.7	1214	2	US-08-231-193A-54	Sequence 54, Appl
706	6	1.7	652	3	US-08-993-775B-36	Sequence 36, Appl	779	6	1.7	1214	2	US-08-486-273A-54	Sequence 54, Appl
707	6	1.7	652	3	US-08-993-775B-38	Sequence 38, Appl	780	6	1.7	1214	2	US-08-480-474-54	Sequence 54, Appl
708	6	1.7	652	3	US-08-993-775B-40	Sequence 40, Appl	781	6	1.7	1214	3	US-08-940-086A-54	Sequence 54, Appl
709	6	1.7	652	3	US-08-993-775B-42	Sequence 42, Appl	782	6	1.7	1214	4	US-08-940-035A-54	Sequence 54, Appl
710	6	1.7	652	3	US-08-993-775B-44	Sequence 44, Appl	783	6	1.7	1214	4	US-08-935-105A-54	Sequence 54, Appl
711	6	1.7	652	3	US-08-993-775B-46	Sequence 46, Appl	784	6	1.7	1214	4	US-09-648-797-54	Sequence 54, Appl
712	6	1.7	652	3	US-08-993-775B-48	Sequence 48, Appl	785	6	1.7	1219	2	US-08-231-193A-50	Sequence 50, Appl
713	6	1.7	652	3	US-08-993-775B-50	Sequence 50, Appl	786	6	1.7	1219	2	US-08-486-273A-50	Sequence 50, Appl
714	6	1.7	652	3	US-08-993-775B-52	Sequence 52, Appl	787	6	1.7	1219	2	US-08-480-474-50	Sequence 50, Appl
715	6	1.7	652	3	US-08-993-775B-54	Sequence 54, Appl	788	6	1.7	1219	3	US-08-940-086A-50	Sequence 50, Appl
716	6	1.7	652	3	US-08-993-775B-56	Sequence 56, Appl	789	6	1.7	1219	4	US-08-940-035A-50	Sequence 50, Appl
717	6	1.7	652	3	US-08-993-775B-58	Sequence 58, Appl	790	6	1.7	1219	4	US-08-935-105A-50	Sequence 50, Appl
718	6	1.7	652	3	US-08-993-775B-60	Sequence 60, Appl	791	6	1.7	1219	4	US-09-648-797-50	Sequence 50, Appl
719	6	1.7	652	3	US-08-993-775B-62	Sequence 62, Appl	792	6	1.7	1231	2	US-08-231-193A-48	Sequence 48, Appl
720	6	1.7	652	3	US-08-993-775B-64	Sequence 64, Appl	793	6	1.7	1231	2	US-08-486-273A-48	Sequence 48, Appl
721	6	1.7	652	3	US-08-993-775B-66	Sequence 66, Appl	794	6	1.7	1231	2	US-08-480-474-48	Sequence 48, Appl
722	6	1.7	652	3	US-08-993-775B-68	Sequence 68, Appl	795	6	1.7	1231	3	US-08-940-086A-48	Sequence 48, Appl
723	6	1.7	652	3	US-08-993-775B-70	Sequence 70, Appl	796	6	1.7	1231	3	US-08-940-035A-48	Sequence 48, Appl
724	6	1.7	652	3	US-08-993-775B-72	Sequence 72, Appl	797	6	1.7	1231	4	US-08-935-105A-48	Sequence 48, Appl
725	6	1.7	652	3	PCT-US92-00040-2	Sequence 2, Appl	798	6	1.7	1231	4	US-09-648-797-48	Sequence 48, Appl
726	6	1.7	652	6	5187091-2	Patent No. 5187091	799	6	1.7	1236	2	US-08-231-193A-6	Sequence 6, Appl
727	6	1.7	653	3	US-08-996-441B-100	Sequence 100, App	800	6	1.7	1236	2	US-08-486-273A-6	Sequence 6, Appl
728	6	1.7	653	3	US-08-993-722A-100	Sequence 100, App	801	6	1.7	1236	3	US-08-480-474-6	Sequence 6, Appl
729	6	1.7	653	3	US-08-993-170A-100	Sequence 100, App	802	6	1.7	1236	3	US-08-940-086A-6	Sequence 6, Appl
730	6	1.7	653	3	US-08-993-775B-100	Sequence 100, App	803	6	1.7	1236	4	US-08-940-035A-6	Sequence 6, Appl
731	6	1.7	654	4	US-08-894-818B-35	Sequence 35, Appl	804	6	1.7	1236	4	US-08-935-105A-6	Sequence 6, Appl
732	6	1.7	654	4	US-09-445-472-16	Sequence 16, Appl	805	6	1.7	1236	4	US-09-648-797-6	Sequence 6, Appl
733	6	1.7	654	4	US-08-894-818B-5	Sequence 5, Appl	806	6	1.7	1239	1	US-08-026-138E-3	Sequence 3, Appl
734	6	1.7	686	4	US-08-982-785A-8	Sequence 8, Appl	807	6	1.7	1239	2	US-08-231-193A-52	Sequence 52, Appl
735	6	1.7	695	1	US-08-127-499A-23	Sequence 23, Appl	808	6	1.7	1239	2	US-08-486-273A-52	Sequence 52, Appl
736	6	1.7	695	1	US-08-482-847-23	Sequence 23, Appl	809	6	1.7	1239	3	US-08-480-474-52	Sequence 52, Appl
737	6	1.7	704	1	US-08-190-802A-62	Sequence 62, Appl	810	6	1.7	1239	3	US-08-940-086A-52	Sequence 52, Appl
738	6	1.7	704	1	US-08-188-582-5	Sequence 5, Appl	811	6	1.7	1239	4	US-08-940-035A-52	Sequence 52, Appl
739	6	1.7	704	1	US-08-646-715-5	Sequence 5, Appl	812	6	1.7	1239	4	US-08-935-105A-52	Sequence 52, Appl
740	6	1.7	704	2	US-08-308-818-3	Sequence 3, Appl	813	6	1.7	1239	4	US-09-648-797-52	Sequence 52, Appl
741	6	1.7	704	4	US-08-477-346-62	Sequence 62, Appl	814	6	1.7	1244	2	US-08-231-193A-46	Sequence 46, Appl
742	6	1.7	704	4	US-08-473-089-62	Sequence 62, Appl	815	6	1.7	1244	2	US-08-486-273A-46	Sequence 46, Appl
743	6	1.7	704	4	US-08-487-072A-62	Sequence 62, Appl	816	6	1.7	1244	3	US-08-480-474-46	Sequence 46, Appl
744	6	1.7	713	1	US-08-453-472-6	Sequence 6, Appl	817	6	1.7	1244	3	US-08-940-086A-46	Sequence 46, Appl
745	6	1.7	713	1	US-08-038-948-7	Sequence 7, Appl	818	6	1.7	1244	4	US-08-940-035A-46	Sequence 46, Appl
746	6	1.7	713	1	US-08-038-948-8	Sequence 8, Appl	819	6	1.7	1244	4	US-08-935-105A-46	Sequence 46, Appl
747	6	1.7	713	1	US-08-038-948-10	Sequence 10, Appl	820	6	1.7	1244	4	US-09-648-797-46	Sequence 46, Appl
748	6	1.7	713	1	US-08-453-952-6	Sequence 6, Appl	821	6	1.7	1313	4	US-09-071-035-450	Sequence 450, App
749	6	1.7	713	2	US-08-862-903-6	Sequence 6, Appl	822	6	1.7	1313	4	US-09-071-035-454	Sequence 454, App
750	6	1.7	726	4	US-08-134-001C-4266	Sequence 4266, Ap	823	6	1.7	1381	4	US-09-540-245A-16	Sequence 16, Appl
751	6	1.7	756	4	US-08-982-785A-2	Sequence 2, Appl	824	6	1.7	1381	4	US-08-826-134-4	Sequence 4, Appl
752	6	1.7	766	2	US-08-846-762-5	Sequence 5, Appl	825	6	1.7	1382	3	US-09-057-570-4	Sequence 2, Appl
753	6	1.7	802	4	US-09-156-316-1	Sequence 1, Appl	826	6	1.7	1384	4	US-08-826-134-2	Sequence 11, Appl
754	6	1.7	802	4	US-09-134-001C-3840	Sequence 3840, Ap	827	6	1.7	1402	4	US-09-004-838-11	Sequence 11, Appl
755	6	1.7	803	1	US-08-158-233-10	Sequence 10, Appl	828	6	1.7	1464	2	US-08-026-138E-1	Sequence 1, Appl
756	6	1.7	803	1	US-08-304-626-10	Sequence 10, Appl	829	6	1.7	1464	2	US-08-231-193A-11	Sequence 11, Appl
757	6	1.7	803	1	US-08-316-301A-12	Sequence 12, Appl	830	6	1.7	1464	2	US-08-486-273A-11	Sequence 11, Appl

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832	6	1.7	1464	4	US-08-436-332B-10	Sequence 10, Appl	905	10	5	US-08-346-333-45	Sequence 45, Appl
833	6	1.7	1464	4	US-08-940-035A-11	Sequence 11, Appl	906	10	5	US-08-617-929-39	Sequence 39, Appl
834	6	1.7	1464	4	US-08-935-105A-11	Sequence 11, Appl	907	10	5	US-08-428-257A-26	Sequence 26, Appl
835	6	1.7	1464	4	US-09-648-797-11	Sequence 11, Appl	908	10	5	US-09-001-984C-78	Sequence 78, Appl
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840	6	1.7	1805	3	US-09-057-570-7	Sequence 7, Appl	913	11	5	US-08-748-021-25	Sequence 25, Appl
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848	6	1.7	3567	2	US-07-642-734C-4	Sequence 4, Appl	921	11	5	US-08-974-297-23	Sequence 23, Appl
849	6	1.7	3567	3	US-08-439-009A-4	Sequence 4, Appl	922	11	5	US-08-974-297-24	Sequence 24, Appl
850	6	1.7	3724	2	US-08-804-227C-10	Sequence 10, Appl	923	11	5	US-08-974-297-25	Sequence 25, Appl
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854	5	1.5	6	1	US-07-718-577-11	Sequence 11, Appl	927	11	5	US-08-974-297-29	Sequence 29, Appl
855	5	1.5	6	1	US-08-179-481-41	Sequence 41, Appl	928	11	5	US-08-974-297-30	Sequence 30, Appl
856	5	1.5	7	2	US-08-705-660-40	Sequence 40, Appl	929	11	5	US-08-974-297-31	Sequence 31, Appl
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858	5	1.5	7	2	US-08-437-013-20	Sequence 20, Appl	931	11	5	5378464-19	Patent No. 5378464
859	5	1.5	7	2	US-08-630-645-25	Sequence 25, Appl	932	11	5	US-07-778-233B-63	Sequence 63, Appl
860	5	1.5	7	2	US-09-174-060-17	Sequence 17, Appl	933	11	5	US-07-963-321-63	Sequence 63, Appl
861	5	1.5	7	3	US-08-989-045-40	Sequence 40, Appl	934	11	5	US-08-290-641-63	Sequence 63, Appl
862	5	1.5	7	3	US-08-338-383-17	Sequence 17, Appl	935	11	5	US-08-548-540-63	Sequence 63, Appl
863	5	1.5	7	4	US-09-258-754-428	Sequence 428, Appl	936	11	5	US-08-406-330-35	Sequence 35, Appl
864	5	1.5	7	4	US-09-042-107-428	Sequence 428, Appl	937	11	5	US-08-737-085A-8	Sequence 8, Appl
865	5	1.5	7	4	PCT-US96-10220-25	Sequence 25, Appl	938	11	5	US-08-737-085A-9	Sequence 9, Appl
866	5	1.5	8	1	US-08-174-365A-32	Sequence 32, Appl	939	11	5	US-08-556-597-35	Sequence 35, Appl
867	5	1.5	8	1	US-08-290-301-74	Sequence 74, Appl	940	11	5	US-08-630-645-24	Sequence 24, Appl
868	5	1.5	8	2	US-08-769-745-32	Sequence 32, Appl	941	11	5	US-08-836-561-36	Sequence 36, Appl
869	5	1.5	8	4	US-08-910-820-21	Sequence 21, Appl	942	11	5	US-09-246-258-8	Sequence 8, Appl
870	5	1.5	8	4	US-09-013-598-74	Sequence 74, Appl	943	11	5	US-09-246-258-9	Sequence 9, Appl
871	5	1.5	8	4	US-08-766-596A-44	Sequence 44, Appl	944	11	5	US-08-660-092-1	Sequence 1, Appl
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875	5	1.5	9	2	US-08-340-283-67	Sequence 67, Appl	948	11	5	US-09-160-513-1	Sequence 1, Appl
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878	5	1.5	9	2	US-08-482-651-8	Sequence 8, Appl	951	11	5	US-08-839-666-9	Sequence 9, Appl
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883	5	1.5	9	2	US-08-845-926-39	Sequence 39, Appl	956	11	5	US-08-726-464B-58	Sequence 58, Appl
884	5	1.5	9	2	US-08-369-643-73	Sequence 73, Appl	957	11	5	US-08-660-092-2	Sequence 2, Appl
885	5	1.5	9	3	US-09-171-705-70	Sequence 70, Appl	958	11	5	US-09-100-930A-25	Sequence 25, Appl
886	5	1.5	9	4	US-08-660-092-9	Sequence 9, Appl	959	11	5	US-09-160-513-2	Sequence 2, Appl
887	5	1.5	9	4	US-08-660-092-11	Sequence 11, Appl	960	11	5	US-08-482-651-1	Sequence 1, Appl
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891	5	1.5	9	4	US-08-660-092-29	Sequence 29, Appl	964	11	5	US-08-660-092-3	Sequence 3, Appl
892	5	1.5	9	4	US-08-660-092-39	Sequence 39, Appl	965	11	5	US-08-660-092-7	Sequence 7, Appl
893	5	1.5	9	4	US-08-660-092-59	Sequence 59, Appl	966	11	5	US-08-660-092-40	Sequence 40, Appl
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897	5	1.5	9	4	US-09-160-513-23	Sequence 23, Appl	970	11	5	US-09-160-513-4	Sequence 4, Appl
898	5	1.5	9	4	US-09-160-513-29	Sequence 29, Appl	971	11	5	US-09-160-513-7	Sequence 7, Appl
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900	5	1.5	9	4	US-09-160-513-39	Sequence 39, Appl	973	11	5	US-09-160-513-224	Sequence 224, Appl
901	5	1.5	9	4	US-09-351-296-39	Sequence 39, Appl	974	11	5	US-08-625-691-3	Sequence 3, Appl
902	5	1.5	9	4	US-08-766-596A-43	Sequence 43, Appl	975	11	5	US-08-408-858A-5	Sequence 5, Appl
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-836-500A-4

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QY 130 SRSEHTGVSVPFAGGVWAVTRDIATRLLEYQWNNIGDAGTGTTRPDNGMLSLGSYSR 188
Db 121 SRSEHTGVSVPFAGGVWAVTRDIATRLLEYQWNNIGDAGTGTTRPDNGMLSLGSYSR 179

RESULT 3
US-08-836-500A-6
; Sequence 6, Application US/08836500A
; Patent No. 6197929
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; APPLICANT: Baussant, Thierry
; APPLICANT: Haeuw, Jean-Francois
; APPLICANT: Nguyen Ngoc, Thien
; TITLE OF INVENTION: Carrier Protein Having an Adjuvant
; TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for
; TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines
; Patent No. 6197929
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Katz, Martin L.
; REGISTRATION NUMBER: 25,011
; REFERENCE/DOCKET NUMBER: P1E1514P0180US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 72 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-836-500A-6

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Best Local Similarity 100.0%; Pred. No. 2.3e-59;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 117 RADSKGNVASTGVSSEHDTGVSVPFAGGVWAVTRDIATRLLEYQWNNIGDAGTGTTRP 176

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-836-500A-8

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QY 136 TGVSPVFAGGVWAVTRDIATRLLEYQWNNIGDAGTGTTRPDNGMLSLGSYSR 188
Db 1 TGVSPVFAGGVWAVTRDIATRLLEYQWNNIGDAGTGTTRPDNGMLSLGSYSR 53

RESULT 5
US-08-457-997B-2
; Sequence 2, Application US/08457997B
; Patent No. 5766608
; GENERAL INFORMATION:
; APPLICANT: Kolattukudy, P. E.
; TITLE OF INVENTION: Otitis Media Vaccine
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter and Griswold
; STREET: Suite 1800 800 Superior Avenue
```

CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457.997B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Golrick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-457-997B-2

Query Match 2.9%; Score 10; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 CLAPDRRVEI 330
DB 344 CLAPDRRVEI 353

RESULT 6
US-08-467-722A-2
Sequence 2, Application US/08467722A
Patent No. 6030626
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467.722A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Golrick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-467-722A-2

Query Match 2.9%; Score 10; DB 3; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 CLAPDRRVEI 330
DB 344 CLAPDRRVEI 353

RESULT 7
US-08-210-394-1
Sequence 1, Application US/08210394
Patent No. 5770213
GENERAL INFORMATION:
APPLICANT: Zlotnick Dr., Gary W.
TITLE OF INVENTION: Purified No. 5770213typable Haemophilus
TITLE OF INVENTION: Influenzae p5 Protein as a Vaccine for No. 5770213typable
TITLE OF INVENTION: Haemophilus Influenzae Strain
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: US
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/210.394
FILING DATE: 07-MAR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J
REFERENCE/DOCKET NUMBER: 32,144
TELEPHONE: 201/831-3246
TELEFAX: 201/831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 338 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-210-394-1

Query Match 2.6%; Score 9; DB 1; Length 338;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 LAPDRRVEI 330
DB 324 LAPDRRVEI 332

RESULT 8
US-08-826-964-2
Sequence 2, Application US/08826964
Patent No. 6033663
GENERAL INFORMATION:
APPLICANT: Ketcham, Catherine M.
TITLE OF INVENTION: Nucleic Acids Encoding GDP-Fucose
TITLE OF INVENTION: Pyrophosphorylase
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,964
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/015,241
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 014137-0099100S
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 594 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-826-964-2

Query Match 2.6%; Score 9; DB 3; Length 594;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 AYNQQLSEK 274
DB 52 AYNQQLSEK 60
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RESULT 9
US-08-920-610-10
; Sequence 10, Application US/08920610
; Patent No. 6015709
; GENERAL INFORMATION:
; APPLICANT: Natesan, Sridaran
; TITLE OF INVENTION: TRANSCRIPTIONAL ACTIVATORS, AND
; TITLE OF INVENTION: COMPOSITIONS AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,610
FILING DATE: 27-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: APV-006.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-920-610-10

Query Match 2.3%; Score 8; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAPAP 206
DB 16 APAPAPAP 23
|||||||

RESULT 10
5252466-19
; Patent No. 5252466
; APPLICANT: CRONAN, JOHN E.
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
; PURIFYING THEM
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/525,568
; FILING DATE: 18-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 354,266
; FILING DATE: 19-MAY-1989
; SEQ ID NO:19:
; LENGTH: 100
5252466-19

Query Match 2.3%; Score 8; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAPAP 206
DB 9 APAPAPAP 16
|||||||

RESULT 11
US-07-956-700B-106
; Sequence 106, Application US/07956700B
; Patent No. 5539092
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5539092th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,700B
FILING DATE: 19921002
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5539092thrup
REGISTRATION NUMBER: 33,268

;; REFERENCE/DOCKET NUMBER: ARCD:058
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 1-312-744-0090
;; TELEFAX: 1-312-755-4489
;; INFORMATION FOR SEQ ID NO: 106:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 165 amino acids
;; TYPE: Amino acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; MOLECULE TYPE: Peptide
US-07-956-700B-106

Query Match 2.3%; Score 8; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAP 206
DB 74 APAPAP 81

RESULT 12

US-08-476-537-106
; Sequence 106, Application US/08476537
; Patent No. 5756290

GENERAL INFORMATION:

;; APPLICANT: Robert Haselkorn and Piotr Gornicki
;; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
;; NUMBER OF SEQUENCES: 116
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60610

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy Disk
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII-DOS
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/476.537
;; FILING DATE:

CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/956,700
;; FILING DATE: 10/21/92

ATTORNEY/AGENT INFORMATION:

;; NAME: Thomas E. No. 5756290thrup
;; REGISTRATION NUMBER: 33,268
;; REFERENCE/DOCKET NUMBER: ARCD:058
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 1-312-744-0090
;; TELEFAX: 1-312-755-4489

INFORMATION FOR SEQ ID NO: 106:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 165 amino acids
;; TYPE: Amino acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; MOLECULE TYPE: Peptide
US-08-476-537-106

Query Match 2.3%; Score 8; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAP 206
DB 74 APAPAP 81

RESULT 13

US-08-485-607-106
; Sequence 106, Application US/08485607
; Patent No. 5792627

GENERAL INFORMATION:

;; APPLICANT: Robert Haselkorn and Piotr Gornicki
;; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
;; NUMBER OF SEQUENCES: 116
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60610

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy Disk
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII-DOS

CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/485.607
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/956,700
;; FILING DATE: 10/21/92

ATTORNEY/AGENT INFORMATION:

;; NAME: Thomas E. No. 5792627thrup
;; REGISTRATION NUMBER: 33,268
;; REFERENCE/DOCKET NUMBER: ARCD:058
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 1-312-744-0090
;; TELEFAX: 1-312-755-4489

INFORMATION FOR SEQ ID NO: 106:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 165 amino acids
;; TYPE: Amino acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; MOLECULE TYPE: Peptide
US-08-485-607-106

Query Match

Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAP 206
DB 74 APAPAP 81

RESULT 14

US-08-475-879-106
; Sequence 106, Application US/08475879
; Patent No. 5972644

GENERAL INFORMATION:

;; APPLICANT: Robert Haselkorn and Piotr Gornicki
;; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
;; NUMBER OF SEQUENCES: 116
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60610

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy Disk
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII-DOS
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/475.879
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/956,700
;; FILING DATE: 10/21/92

ATTORNEY/AGENT INFORMATION:

;; NAME: Thomas E. No. 5972644
;; REGISTRATION NUMBER: 33,268
;; REFERENCE/DOCKET NUMBER: ARCD:058
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 1-312-744-0090
;; TELEFAX: 1-312-755-4489

INFORMATION FOR SEQ ID NO: 106:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 165 amino acids
;; TYPE: Amino acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; MOLECULE TYPE: Peptide
US-08-475-879-106

Query Match

Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAP 206
DB 74 APAPAP 81

MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,879
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5972644 5786170thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-312-744-0090
TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: Amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-475-879-106

Query Match 2.3%; Score 8; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAP 206
Db 74 APAPAP 81

RESULT 15
US-09-433-043B-106
Sequence 106, Application US/09433043B
Patent No. 6399342
GENERAL INFORMATION:
APPLICANT: HASELKORN, ROBERT
APPLICANT: GORNICKI, PIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE REFERENCE: ARCD:338US
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/475,879
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/956,700
PRIOR FILING DATE: 1992-10-02
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 106
LENGTH: 165
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-433-043B-106

Query Match 2.3%; Score 8; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAP 206
Db 74 APAPAP 81

Search completed: April 15, 2003, 08:56:53
Job time: 30 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 08:56:35 ; Search time 20 Seconds
(without alignments)
1051.540 Million cell updates/sec

Title: US-09-831-061-2

Perfect score: 344

Sequence: 1 MKAIFVLNAPKONTWYAGG.....DRVEIEVKGKVVYTPAG 344

Scoring table: OLIGO

.Gapop 60.0 , Gapext 60.0

Searched: 248812 seqs, 61136040 residues

Word size : 5

Total number of hits satisfying chosen parameters: 11432

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published_Applications_AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US05_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	33	9.6	153	10	US-09-905-176-22
3	8	2.3	25	9	US-09-922-199A-15
4	8	2.3	60	10	US-09-864-761-38830
5	8	2.3	66	9	US-09-922-199A-14
6	8	2.3	191	9	US-09-738-626-3880
7	8	2.3	269	10	US-09-965-703-54
8	8	2.3	283	12	US-10-042-417-50
9	8	2.3	332	9	US-09-764-868-1040
10	8	2.3	516	9	US-09-291-417-6
11	8	2.3	547	10	US-09-771-161A-272
12	8	2.3	547	10	US-09-771-161A-273
13	8	2.3	670	9	US-09-298-523B-63
14	8	2.3	701	9	US-09-298-523B-62
15	8	2.3	707	9	US-09-298-523B-3
16	8	2.3	711	9	US-09-298-523B-2
17	8	2.3	891	9	US-09-976-059-18
18	7	2.0	95	9	US-09-834-794A-21
19	7	2.0	95	10	US-09-834-795A-21

20	7	2.0	96	9	US-10-164-621-2	Sequence 2, Appli
21	7	2.0	96	9	US-10-125-451-2	Sequence 2, Appli
22	7	2.0	96	9	US-10-146-496-10	Sequence 10, Appli
23	7	2.0	96	10	US-09-988-598-2606	Sequence 2606, Ap
24	7	2.0	111	10	US-09-864-761-39500	Sequence 39500, A
25	7	2.0	113	10	US-09-864-761-39507	Sequence 39507, A
26	7	2.0	121	10	US-09-764-864-1125	Sequence 1125, A
27	7	2.0	128	10	US-09-864-761-35942	Sequence 35942, A
28	7	2.0	132	12	US-10-078-929-22	Sequence 22, Appl
29	7	2.0	132	12	US-10-078-929-198	Sequence 198, App
30	7	2.0	155	10	US-09-815-242-11159	Sequence 11159, A
31	7	2.0	178	9	US-09-965-528-16	Sequence 16, Appl
32	7	2.0	255	10	US-09-897-214-2	Sequence 2, Appli
33	7	2.0	255	10	US-09-893-717-232	Sequence 232, App
34	7	2.0	283	9	US-10-091-483-320	Sequence 220, App
35	7	2.0	283	10	US-09-764-846-220	Sequence 220, App
36	7	2.0	286	9	US-09-985-372-4	Sequence 4, Appli
37	7	2.0	312	9	US-09-995-634-134	Sequence 134, App
38	7	2.0	312	9	US-09-997-181-134	Sequence 134, App
39	7	2.0	312	9	US-09-997-182-134	Sequence 134, App
40	7	2.0	322	10	US-09-789-836-6	Sequence 6, Appli
41	7	2.0	325	9	US-09-985-372-2	Sequence 2, Appli
42	7	2.0	325	9	US-09-985-372-3	Sequence 3, Appli
43	7	2.0	337	10	US-09-826-752-12	Sequence 12, Appl
44	7	2.0	345	10	US-09-789-836-5	Sequence 5, Appli
45	7	2.0	348	10	US-09-982-610-18	Sequence 18, Appl
46	7	2.0	361	10	US-09-955-518-21	Sequence 21, Appl
47	7	2.0	374	10	US-09-888-615-61	Sequence 61, Appl
48	7	2.0	477	9	US-10-091-483-140	Sequence 140, App
49	7	2.0	477	10	US-09-764-846-140	Sequence 140, App
50	7	2.0	587	10	US-09-815-242-12082	Sequence 12082, A
51	7	2.0	617	10	US-09-817-676A-12	Sequence 12, Appl
52	7	2.0	631	10	US-09-841-132-325	Sequence 325, App
53	7	2.0	640	10	US-09-918-951-4	Sequence 4, Appli
54	7	2.0	693	9	US-10-029-217A-4	Sequence 4, Appli
55	7	2.0	766	10	US-09-801-368-316	Sequence 316, App
56	7	2.0	802	10	US-09-287-849-10	Sequence 10, Appl
57	7	2.0	902	9	US-09-922-199A-2	Sequence 2, Appli
58	7	2.0	972	10	US-09-944-807-10	Sequence 10, Appl
59	7	2.0	976	9	US-10-099-895-32	Sequence 32, Appl
60	7	2.0	1016	12	US-10-007-693-95	Sequence 95, Appl
61	7	2.0	1023	9	US-09-893-519A-14	Sequence 14, Appl
62	7	2.0	1298	10	US-09-982-610-33	Sequence 33, Appl
63	7	2.0	1363	9	US-09-375-248-2	Sequence 2, Appli
64	7	2.0	1618	9	US-09-963-875-1	Sequence 1, Appli
65	7	2.0	1618	9	US-10-136-891-2	Sequence 2, Appli
66	7	2.0	2665	10	US-09-864-761-34248	Sequence 34248, A
67	6	1.7	9	9	US-09-277-074-19	Sequence 19, Appl
68	6	1.7	10	8	US-08-452-843A-14	Sequence 14, Appl
69	6	1.7	10	9	US-09-017-743C-117	Sequence 117, App
70	6	1.7	11	9	US-09-277-074-18	Sequence 18, Appl
71	6	1.7	12	10	US-09-943-692-47	Sequence 47, Appl
72	6	1.7	15	10	US-09-943-692-3	Sequence 3, Appli
73	6	1.7	16	9	US-10-002-344A-216	Sequence 216, App
74	6	1.7	29	9	US-10-214-188-12	Sequence 12, Appl
75	6	1.7	42	10	US-09-864-761-35506	Sequence 35506, A
76	6	1.7	58	9	US-10-003-392-12	Sequence 12, Appl
77	6	1.7	58	10	US-09-864-761-39842	Sequence 39842, A
78	6	1.7	63	9	US-10-001-354-56	Sequence 56, Appl
79	6	1.7	69	10	US-09-764-860-438	Sequence 438, App
80	6	1.7	75	10	US-09-867-550-652	Sequence 652, App
81	6	1.7	76	10	US-09-738-626-5670	Sequence 5670, Ap
82	6	1.7	76	10	US-09-925-297-476	Sequence 476, App
83	6	1.7	89	10	US-09-881-752A-114	Sequence 114, App
84	6	1.7	93	9	US-10-102-806-616	Sequence 616, App
85	6	1.7	93	10	US-09-864-761-36770	Sequence 36770, A
86	6	1.7	102	10	US-09-823-038A-34	Sequence 34, Appl
87	6	1.7	109	9	US-10-081-817-28	Sequence 28, Appl
88	6	1.7	113	9	US-10-051-643-140	Sequence 140, App
89	6	1.7	113	9	US-09-880-505-140	Sequence 140, App
90	6	1.7	114	10	US-09-974-449-8	Sequence 8, Appli
91	6	1.7	118	9	US-09-925-299-1033	Sequence 1033, Ap
92	6	1.7	118	10	US-09-925-299-1033	Sequence 1033, Ap

93	6	1.7	122	9	US-10-091-504-814	Sequence 834, App	166	6	1.7	302	10	US-09-935-943-8	Sequence 8, Appl1
94	6	1.7	122	10	US-09-764-869-814	Sequence 814, App	167	6	1.7	310	10	US-09-886-055-485	Sequence 485, App
95	6	1.7	132	9	US-09-981-876-147	Sequence 147, App	168	6	1.7	315	10	US-09-983-306-3	Sequence 3, Appl1
96	6	1.7	132	9	US-09-148-845-147	Sequence 147, App	169	6	1.7	315	10	US-09-983-306-6	Sequence 6, Appl1
97	6	1.7	133	9	US-10-128-540-524	Sequence 524, App	170	6	1.7	316	9	US-10-017-910-4	Sequence 4, Appl1
98	6	1.7	133	10	US-09-764-870-524	Sequence 524, App	171	6	1.7	316	9	US-10-105-057-2	Sequence 2, Appl1
99	6	1.7	133	10	US-09-908-711-90	Sequence 90, Appl	172	6	1.7	316	10	US-09-815-242-5784	Sequence 5784, App
100	6	1.7	139	9	US-09-712-363-235	Sequence 235, App	173	6	1.7	319	9	US-09-968-851-42	Sequence 42, Appl1
101	6	1.7	140	10	US-09-764-887-289	Sequence 289, App	174	6	1.7	321	9	US-09-738-628-486	Sequence 486, App
102	6	1.7	143	8	US-08-981-087A-4	Sequence 4, Appl1	175	6	1.7	321	9	US-10-051-643-182	Sequence 182, App
103	6	1.7	147	10	US-09-823-038A-35	Sequence 35, Appl	176	6	1.7	331	9	US-09-880-505-182	Sequence 182, App
104	6	1.7	152	10	US-09-777-558-6	Sequence 6, Appl1	177	6	1.7	331	9	US-09-738-626-4771	Sequence 4771, App
105	6	1.7	162	10	US-09-800-528-2	Sequence 2, Appl1	178	6	1.7	335	10	US-09-968-851-44	Sequence 44, Appl
106	6	1.7	164	10	US-09-925-300-1451	Sequence 1451, App	179	6	1.7	335	10	US-09-815-242-12780	Sequence 12780, A
107	6	1.7	168	10	US-09-815-242-5440	Sequence 5440, App	180	6	1.7	335	10	US-09-815-242-13125	Sequence 13125, A
108	6	1.7	170	10	US-09-818-066-42	Sequence 42, App	181	6	1.7	337	9	US-10-063-547-74	Sequence 74, Appl
109	6	1.7	172	10	US-09-777-558-14	Sequence 14, Appl	182	6	1.7	337	9	US-09-738-626-3997	Sequence 3997, App
110	6	1.7	173	10	US-09-800-528-13	Sequence 13, Appl	183	6	1.7	337	9	US-10-174-590-268	Sequence 268, App
111	6	1.7	173	10	US-09-815-242-12386	Sequence 12386, A	184	6	1.7	337	9	US-10-176-758-268	Sequence 268, App
112	6	1.7	173	10	US-09-815-242-12822	Sequence 12822, A	185	6	1.7	337	9	US-10-063-616-74	Sequence 74, Appl
113	6	1.7	173	10	US-09-815-242-13135	Sequence 13135, A	186	6	1.7	337	9	US-10-175-737-268	Sequence 268, App
114	6	1.7	174	10	US-09-818-066-42	Sequence 42, App	187	6	1.7	337	9	US-10-063-502-74	Sequence 74, Appl
115	6	1.7	174	10	US-09-818-066-43	Sequence 43, Appl	188	6	1.7	337	9	US-10-173-706-268	Sequence 268, App
116	6	1.7	174	10	US-09-818-066-45	Sequence 45, Appl	189	6	1.7	337	9	US-10-175-738-268	Sequence 268, App
117	6	1.7	174	10	US-09-818-066-46	Sequence 46, Appl	190	6	1.7	337	9	US-10-175-752-268	Sequence 268, App
118	6	1.7	174	10	US-09-818-066-47	Sequence 47, Appl	191	6	1.7	337	9	US-10-176-482-268	Sequence 268, App
119	6	1.7	174	10	US-09-818-066-48	Sequence 48, Appl	192	6	1.7	337	9	US-10-176-757-268	Sequence 268, App
120	6	1.7	174	10	US-09-818-066-50	Sequence 50, Appl	193	6	1.7	337	9	US-10-176-913-268	Sequence 268, App
121	6	1.7	174	10	US-09-818-066-51	Sequence 51, Appl	194	6	1.7	337	9	US-10-180-552-268	Sequence 268, App
122	6	1.7	174	10	US-09-818-066-52	Sequence 52, Appl	195	6	1.7	337	9	US-10-180-557-268	Sequence 268, App
123	6	1.7	174	10	US-09-818-066-53	Sequence 53, Appl	196	6	1.7	337	9	US-10-173-700-268	Sequence 268, App
124	6	1.7	174	10	US-09-818-066-54	Sequence 54, Appl	197	6	1.7	337	9	US-10-174-572-268	Sequence 268, App
125	6	1.7	174	10	US-09-818-066-55	Sequence 55, Appl	198	6	1.7	337	9	US-10-174-579-268	Sequence 268, App
126	6	1.7	174	10	US-09-818-066-56	Sequence 56, Appl	199	6	1.7	337	9	US-10-174-582-268	Sequence 268, App
127	6	1.7	174	10	US-09-818-066-57	Sequence 57, Appl	200	6	1.7	337	9	US-10-174-588-268	Sequence 268, App
128	6	1.7	174	10	US-09-818-066-62	Sequence 62, Appl	201	6	1.7	337	9	US-10-175-739-268	Sequence 268, App
129	6	1.7	174	10	US-09-864-761-48360	Sequence 48360, A	202	6	1.7	337	9	US-10-175-740-268	Sequence 268, App
130	6	1.7	193	10	US-09-864-761-37748	Sequence 37748, A	203	6	1.7	337	9	US-10-175-743-268	Sequence 268, App
131	6	1.7	194	10	US-09-967-347-8	Sequence 8, Appl1	204	6	1.7	337	9	US-10-176-488-268	Sequence 268, App
132	6	1.7	205	9	US-09-738-626-3591	Sequence 3591, App	205	6	1.7	337	9	US-10-176-492-268	Sequence 268, App
133	6	1.7	207	9	US-09-738-626-4510	Sequence 4510, App	206	6	1.7	337	9	US-10-176-747-268	Sequence 268, App
134	6	1.7	208	9	US-09-738-626-6854	Sequence 6854, App	207	6	1.7	337	9	US-10-176-750-268	Sequence 268, App
135	6	1.7	215	9	US-09-764-868-1004	Sequence 1004, App	208	6	1.7	337	9	US-10-176-985-268	Sequence 268, App
136	6	1.7	219	10	US-09-974-449-38	Sequence 38, Appl	209	6	1.7	337	9	US-10-176-987-268	Sequence 268, App
137	6	1.7	223	10	US-09-970-711-11	Sequence 11, Appl	210	6	1.7	337	9	US-10-176-991-268	Sequence 268, App
138	6	1.7	224	9	US-10-001-254-57	Sequence 57, Appl	211	6	1.7	337	9	US-10-176-992-268	Sequence 268, App
139	6	1.7	224	10	US-09-841-132-397	Sequence 397, App	212	6	1.7	337	9	US-10-176-993-268	Sequence 268, App
140	6	1.7	224	10	US-09-841-132-508	Sequence 508, App	213	6	1.7	337	9	US-10-184-658-268	Sequence 268, App
141	6	1.7	234	10	US-09-939-980-517	Sequence 517, App	214	6	1.7	337	9	US-10-173-695-268	Sequence 268, App
142	6	1.7	240	9	US-09-880-748-1918	Sequence 1918, App	215	6	1.7	337	9	US-10-173-697-268	Sequence 268, App
143	6	1.7	240	10	US-09-815-242-13469	Sequence 13469, A	216	6	1.7	337	9	US-10-173-705-268	Sequence 268, App
144	6	1.7	241	10	US-09-819-917-5	Sequence 5, Appl1	217	6	1.7	337	9	US-10-174-576-268	Sequence 268, App
145	6	1.7	246	9	US-09-738-626-5858	Sequence 5858, App	218	6	1.7	337	9	US-10-174-585-268	Sequence 268, App
146	6	1.7	253	9	US-09-968-851-30	Sequence 30, Appl	219	6	1.7	337	9	US-10-174-586-268	Sequence 268, App
147	6	1.7	253	9	US-09-738-626-4362	Sequence 4362, App	220	6	1.7	337	9	US-10-173-747-268	Sequence 268, App
148	6	1.7	257	9	US-09-924-900-6	Sequence 6, Appl1	221	6	1.7	337	9	US-10-176-481-268	Sequence 268, App
149	6	1.7	262	9	US-09-764-868-644	Sequence 644, App	222	6	1.7	337	9	US-10-176-485-268	Sequence 268, App
150	6	1.7	264	9	US-10-043-487-254	Sequence 254, App	223	6	1.7	337	9	US-10-176-487-268	Sequence 268, App
151	6	1.7	267	9	US-09-981-353-82	Sequence 82, Appl	224	6	1.7	337	9	US-10-176-493-268	Sequence 268, App
152	6	1.7	269	10	US-09-777-558-17	Sequence 17, Appl	225	6	1.7	337	9	US-10-176-756-268	Sequence 268, App
153	6	1.7	270	9	US-09-968-851-32	Sequence 32, Appl	226	6	1.7	337	9	US-10-176-911-268	Sequence 268, App
154	6	1.7	270	10	US-09-925-301-1205	Sequence 1205, App	227	6	1.7	337	9	US-10-176-919-268	Sequence 268, App
155	6	1.7	273	9	US-09-738-626-4392	Sequence 4392, App	228	6	1.7	337	9	US-10-176-925-268	Sequence 268, App
156	6	1.7	273	10	US-09-900-575-40	Sequence 40, Appl	229	6	1.7	337	9	US-10-176-978-268	Sequence 268, App
157	6	1.7	280	10	US-09-983-306-1	Sequence 1, Appl1	230	6	1.7	337	9	US-10-179-510-268	Sequence 268, App
158	6	1.7	283	9	US-09-738-626-3533	Sequence 3533, App	231	6	1.7	337	9	US-10-180-543-268	Sequence 268, App
159	6	1.7	293	9	US-09-946-406-6	Sequence 6, Appl1	232	6	1.7	337	9	US-10-180-544-268	Sequence 268, App
160	6	1.7	294	9	US-09-877-650-11	Sequence 11, Appl	233	6	1.7	337	9	US-10-180-546-268	Sequence 268, App
161	6	1.7	294	10	US-09-871-856-11	Sequence 11, Appl	234	6	1.7	337	9	US-10-180-547-268	Sequence 268, App
162	6	1.7	295	9	US-10-106-534-4	Sequence 4, Appl1	235	6	1.7	337	9	US-10-180-549-268	Sequence 268, App
163	6	1.7	297	10	US-09-925-297-635	Sequence 635, App	236	6	1.7	337	9	US-10-180-555-268	Sequence 268, App
164	6	1.7	299	10	US-09-739-254-73	Sequence 73, Appl	237	6	1.7	337	9	US-10-180-559-268	Sequence 268, App
165	6	1.7	299	10	US-09-904-615-73	Sequence 73, Appl	238	6	1.7	337	9	US-10-181-000-268	Sequence 268, App

385	6	1.7	337	9	US-10-201-534-268	Sequence 268, App	458	6	1.7	350	9	US-09-906-838-236	Sequence 236, App
386	6	1.7	337	9	US-10-201-770-268	Sequence 268, App	459	6	1.7	350	9	US-09-907-813-236	Sequence 236, App
387	6	1.7	337	9	US-10-201-855-268	Sequence 268, App	460	6	1.7	350	9	US-09-907-942-236	Sequence 236, App
388	6	1.7	337	9	US-10-201-855-268	Sequence 268, App	461	6	1.7	350	9	US-09-904-820-236	Sequence 236, App
389	6	1.7	337	9	US-10-202-469-268	Sequence 268, App	462	6	1.7	350	9	US-09-904-859-236	Sequence 236, App
390	6	1.7	337	9	US-10-202-470-268	Sequence 268, App	463	6	1.7	350	9	US-09-909-204-236	Sequence 236, App
391	6	1.7	337	9	US-10-202-476-268	Sequence 268, App	464	6	1.7	350	9	US-09-904-786-236	Sequence 236, App
392	6	1.7	337	9	US-10-202-934-268	Sequence 268, App	465	6	1.7	350	9	US-09-906-646-236	Sequence 236, App
393	6	1.7	337	9	US-10-202-935-268	Sequence 268, App	466	6	1.7	350	9	US-09-906-700-236	Sequence 236, App
394	6	1.7	337	9	US-10-202-936-268	Sequence 268, App	467	6	1.7	350	9	US-09-902-903-236	Sequence 236, App
395	6	1.7	337	9	US-10-202-939-268	Sequence 268, App	468	6	1.7	350	9	US-09-903-749A-236	Sequence 236, App
396	6	1.7	337	9	US-10-205-504-268	Sequence 268, App	469	6	1.7	350	9	US-09-903-786-236	Sequence 236, App
397	6	1.7	337	9	US-10-205-509-268	Sequence 268, App	470	6	1.7	350	9	US-09-902-736-236	Sequence 236, App
398	6	1.7	337	9	US-10-205-895-268	Sequence 268, App	471	6	1.7	350	9	US-09-904-119-236	Sequence 236, App
399	6	1.7	337	9	US-10-205-895-268	Sequence 268, App	472	6	1.7	350	9	US-09-904-956-236	Sequence 236, App
400	6	1.7	337	9	US-10-205-899-268	Sequence 268, App	473	6	1.7	350	9	US-09-907-794-236	Sequence 236, App
401	6	1.7	337	9	US-10-205-909-268	Sequence 268, App	474	6	1.7	350	9	US-10-063-518-8	Sequence 8, Appl
402	6	1.7	337	9	US-10-227-693-74	Sequence 74, Appl	475	6	1.7	350	9	US-10-063-598-8	Sequence 8, Appl
403	6	1.7	337	9	US-10-006-818A-423	Sequence 423, App	476	6	1.7	350	9	US-10-227-693-8	Sequence 8, Appl
404	6	1.7	337	9	US-10-183-002-268	Sequence 268, App	477	6	1.7	350	9	US-09-902-692-236	Sequence 236, App
405	6	1.7	337	9	US-10-184-621-268	Sequence 268, App	478	6	1.7	350	9	US-09-903-520-236	Sequence 236, App
406	6	1.7	337	9	US-10-184-638-268	Sequence 268, App	479	6	1.7	350	9	US-09-903-943-236	Sequence 236, App
407	6	1.7	337	9	US-10-187-752-268	Sequence 268, App	480	6	1.7	350	9	US-09-904-462-236	Sequence 236, App
408	6	1.7	337	9	US-10-187-887-268	Sequence 268, App	481	6	1.7	350	9	US-09-905-056-236	Sequence 236, App
409	6	1.7	337	9	US-10-194-461-268	Sequence 268, App	482	6	1.7	350	9	US-09-907-925-236	Sequence 236, App
410	6	1.7	337	9	US-10-195-892-268	Sequence 268, App	483	6	1.7	350	9	US-09-904-553-236	Sequence 236, App
411	6	1.7	337	9	US-10-196-751-268	Sequence 268, App	484	6	1.7	350	9	US-09-905-381-236	Sequence 236, App
412	6	1.7	337	9	US-10-197-694-268	Sequence 268, App	485	6	1.7	350	10	US-09-909-064-236	Sequence 236, App
413	6	1.7	337	9	US-10-197-697-268	Sequence 268, App	486	6	1.7	350	10	US-09-909-320-236	Sequence 236, App
414	6	1.7	337	9	US-10-197-707-268	Sequence 268, App	487	6	1.7	350	10	US-09-909-088B-236	Sequence 236, App
415	6	1.7	337	9	US-10-199-303-268	Sequence 268, App	488	6	1.7	350	12	US-10-006-867-8	Sequence 8, Appl
416	6	1.7	337	9	US-10-199-318-268	Sequence 268, App	489	6	1.7	351	10	US-09-923-301-1426	Sequence 1426, Ap
417	6	1.7	337	9	US-10-199-458-268	Sequence 268, App	490	6	1.7	353	9	US-09-968-851-40	Sequence 40, Appl
418	6	1.7	337	9	US-10-199-462-268	Sequence 268, App	491	6	1.7	353	9	US-09-738-626-3982	Sequence 3982, Ap
419	6	1.7	337	9	US-10-201-324-268	Sequence 268, App	492	6	1.7	358	9	US-09-893-519A-13	Sequence 13, Appl
420	6	1.7	337	9	US-10-201-328-268	Sequence 268, App	493	6	1.7	360	10	US-09-815-242-12094	Sequence 12094, A
421	6	1.7	337	9	US-10-201-527-268	Sequence 268, App	494	6	1.7	363	9	US-09-968-851-26	Sequence 26, Appl
422	6	1.7	337	9	US-10-201-528-268	Sequence 268, App	495	6	1.7	365	10	US-09-815-242-11972	Sequence 11972, A
423	6	1.7	337	9	US-10-201-529-268	Sequence 268, App	496	6	1.7	373	10	US-09-789-386-6	Sequence 6, Appl
424	6	1.7	337	9	US-10-205-502-268	Sequence 268, App	497	6	1.7	373	10	US-08-785-205-6	Sequence 6, Appl
425	6	1.7	337	9	US-10-205-511-268	Sequence 268, App	498	6	1.7	373	10	US-09-893-348-24	Sequence 24, Appl
426	6	1.7	337	9	US-10-205-902-268	Sequence 268, App	499	6	1.7	373	12	US-10-109-860-2	Sequence 2, Appl
427	6	1.7	337	9	US-10-202-409-268	Sequence 268, App	500	6	1.7	374	9	US-09-968-851-28	Sequence 28, Appl
428	6	1.7	337	9	US-10-202-411-268	Sequence 268, App	501	6	1.7	374	9	US-09-934-900-19	Sequence 19, Appl
429	6	1.7	337	9	US-10-202-472-268	Sequence 268, App	502	6	1.7	380	9	US-09-934-900-12	Sequence 12, Appl
430	6	1.7	337	9	US-10-205-507-268	Sequence 268, App	503	6	1.7	381	9	US-09-808-602-6	Sequence 6, Appl
431	6	1.7	337	9	US-10-205-507-268	Sequence 268, App	504	6	1.7	381	9	US-09-968-851-36	Sequence 36, Appl
432	6	1.7	337	9	US-10-205-511-268	Sequence 268, App	505	6	1.7	381	9	US-09-977-418-22	Sequence 22, Appl
433	6	1.7	337	9	US-10-205-907-268	Sequence 268, App	506	6	1.7	381	9	US-09-934-900-16	Sequence 16, Appl
434	6	1.7	337	9	US-10-194-456-268	Sequence 268, App	507	6	1.7	383	9	US-09-908-504A-1	Sequence 1, Appl
435	6	1.7	337	9	US-10-196-758-268	Sequence 268, App	508	6	1.7	383	10	US-09-771-956-27	Sequence 27, Appl
436	6	1.7	337	9	US-10-198-770-268	Sequence 268, App	509	6	1.7	383	10	US-09-912-020-265	Sequence 265, App
437	6	1.7	337	9	US-10-199-308-268	Sequence 268, App	510	6	1.7	383	10	US-09-815-242-10033	Sequence 10033, A
438	6	1.7	337	9	US-10-200-617-268	Sequence 268, App	511	6	1.7	384	9	US-09-934-900-17	Sequence 17, Appl
439	6	1.7	337	9	US-10-205-893-268	Sequence 268, App	512	6	1.7	388	10	US-09-925-300-1618	Sequence 1618, Ap
440	6	1.7	337	9	US-10-205-897-268	Sequence 268, App	513	6	1.7	389	9	US-09-821-877-2	Sequence 2, Appl
441	6	1.7	337	10	US-09-946-143-2	Sequence 2, Appl	514	6	1.7	390	10	US-09-815-242-5770	Sequence 5770, Ap
442	6	1.7	337	12	US-10-006-867-74	Sequence 74, Appl	515	6	1.7	392	10	US-09-815-242-12723	Sequence 12723, A
443	6	1.7	337	12	US-10-052-586-268	Sequence 268, App	516	6	1.7	393	9	US-09-029-327-4	Sequence 4, Appl
444	6	1.7	340	9	US-10-013-477-14	Sequence 14, Appl	517	6	1.7	393	10	US-09-776-695-32	Sequence 32, Appl
445	6	1.7	341	10	US-09-771-956-26	Sequence 26, Appl	518	6	1.7	393	10	US-09-732-384-3	Sequence 3, Appl
446	6	1.7	342	9	US-10-001-857-201	Sequence 201, Appl	519	6	1.7	393	10	US-09-860-211-9	Sequence 9, Appl
447	6	1.7	350	9	US-09-905-291A-236	Sequence 236, App	520	6	1.7	394	12	US-10-155-059-4	Sequence 4, Appl
448	6	1.7	350	9	US-09-976-736-9	Sequence 9, Appl	521	6	1.7	396	9	US-09-934-900-18	Sequence 18, Appl
449	6	1.7	350	9	US-10-063-547-8	Sequence 8, Appl	522	6	1.7	396	9	US-09-934-900-22	Sequence 22, Appl
450	6	1.7	350	9	US-09-902-853-236	Sequence 236, App	523	6	1.7	398	9	US-09-738-626-6516	Sequence 6516, Ap
451	6	1.7	350	9	US-09-907-824-236	Sequence 236, App	524	6	1.7	398	9	US-10-081-816-19	Sequence 19, Appl
452	6	1.7	350	9	US-09-907-841-236	Sequence 236, App	525	6	1.7	398	9	US-09-934-900-20	Sequence 20, Appl
453	6	1.7	350	9	US-09-904-011-236	Sequence 236, App	526	6	1.7	398	10	US-09-912-020-304	Sequence 304, App
454	6	1.7	350	9	US-10-201-310-2	Sequence 2, Appl	527	6	1.7	398	10	US-09-731-872-288	Sequence 288, App
455	6	1.7	350	9	US-10-063-616-8	Sequence 8, Appl	528	6	1.7	399	9	US-09-764-868-850	Sequence 850, App
456	6	1.7	350	9	US-09-906-742-236	Sequence 236, App	529	6	1.7	401	9	US-09-968-851-34	Sequence 34, Appl
457	6	1.7	350	9	US-10-063-503-8	Sequence 8, Appl	530	6	1.7	401	9	US-09-738-626-3705	Sequence 3705, Ap

531	6	1.7	401	9	US-09-738-626-5923	604	597	9	US-09-997-182-129	Sequence 129, App
532	6	1.7	401	9	US-09-738-626-6636	605	600	9	US-10-003-392-20	Sequence 20, Appl
533	6	1.7	402	10	US-09-854-731-16	606	605	9	US-10-128-870-24	Sequence 24, Appl
534	6	1.7	403	10	US-09-731-872-249	607	605	9	US-10-131-685-24	Sequence 24, Appl
535	6	1.7	403	9	US-09-934-900-2	608	615	9	US-09-908-193-26	Sequence 26, Appl
536	6	1.7	408	9	US-10-102-806-639	609	615	9	US-09-908-193-27	Sequence 27, Appl
537	6	1.7	408	12	US-10-109-860-4	610	619	9	US-09-882-774-1	Sequence 1, Appl
538	6	1.7	410	10	US-09-866-562-41	611	641	10	US-10-267-311-51	Sequence 51, Appl
539	6	1.7	410	10	US-09-815-242-10639	612	641	10	US-09-876-527-2	Sequence 2, Appl
540	6	1.7	411	10	US-09-815-242-4909	613	644	10	US-10-222-441-2	Sequence 2, Appl
541	6	1.7	412	12	US-10-090-624-1	614	644	10	US-09-943-692-2	Sequence 2, Appl
542	6	1.7	413	10	US-09-919-703-12	615	654	12	US-10-080-624-16	Sequence 16, Appl
543	6	1.7	416	10	US-09-815-242-11301	616	672	9	US-09-928-530-5	Sequence 5, Appl
544	6	1.7	416	10	US-09-881-752A-172	617	672	9	US-10-162-012-30	Sequence 30, Appl
545	6	1.7	421	10	US-09-815-242-11192	618	674	9	US-10-028-072-36	Sequence 36, Appl
546	6	1.7	423	10	US-09-815-242-10566	619	674	9	US-10-121-049-36	Sequence 36, Appl
547	6	1.7	425	9	US-09-738-626-4016	620	674	9	US-10-121-049-36	Sequence 36, Appl
548	6	1.7	427	9	US-09-764-868-894	621	674	9	US-10-140-470-36	Sequence 36, Appl
549	6	1.7	428	9	US-09-906-514-4	622	674	9	US-10-173-746-36	Sequence 36, Appl
550	6	1.7	429	9	US-09-738-626-5628	623	674	9	US-10-176-918-36	Sequence 36, Appl
551	6	1.7	431	8	US-08-981-087A-1	624	674	9	US-10-176-921-36	Sequence 36, Appl
552	6	1.7	432	9	US-09-910-186A-16	625	674	9	US-10-137-865-36	Sequence 36, Appl
553	6	1.7	432	9	US-09-910-186A-34	626	674	9	US-10-140-474-36	Sequence 36, Appl
554	6	1.7	432	10	US-09-815-242-10566	627	674	9	US-10-140-474-36	Sequence 36, Appl
555	6	1.7	433	9	US-09-906-514-2	628	674	9	US-10-142-431-36	Sequence 36, Appl
556	6	1.7	442	9	US-09-738-626-5860	629	674	9	US-10-143-114-36	Sequence 36, Appl
557	6	1.7	446	9	US-09-866-570A-74	630	674	9	US-10-140-002-36	Sequence 36, Appl
558	6	1.7	446	10	US-09-866-572A-74	631	674	9	US-10-142-419-36	Sequence 36, Appl
559	6	1.7	448	10	US-09-871-212-8	632	674	9	US-10-123-262-36	Sequence 36, Appl
560	6	1.7	456	10	US-09-323-998D-20	633	674	9	US-10-142-423-36	Sequence 36, Appl
561	6	1.7	461	12	US-10-013-823-3	634	674	9	US-10-121-050-36	Sequence 36, Appl
562	6	1.7	462	10	US-09-745-763-189	635	674	9	US-10-141-755-36	Sequence 36, Appl
563	6	1.7	471	9	US-10-003-392-10	636	674	9	US-10-143-032-36	Sequence 36, Appl
564	6	1.7	477	9	US-09-738-626-6985	637	689	9	US-09-738-626-3675	Sequence 36, Appl
565	6	1.7	478	9	US-09-924-340-108	638	690	9	US-09-298-523B-61	Sequence 61, Appl
566	6	1.7	478	9	US-09-992-600A-108	639	691	8	US-08-834-666A-12	Sequence 12, Appl
567	6	1.7	478	9	US-09-746-783-184	640	691	8	US-08-834-666A-22	Sequence 22, Appl
568	6	1.7	484	9	US-10-212-933-4	641	691	8	US-09-298-523B-1	Sequence 1, Appl
569	6	1.7	486	10	US-09-793-848A-4	642	716	10	US-09-815-242-12403	Sequence 12403, A
570	6	1.7	487	9	US-10-023-437-19	643	717	9	US-10-101-64A-810	Sequence 810, App
571	6	1.7	488	10	US-09-801-196-26	644	722	10	US-09-815-242-11000	Sequence 11000, A
572	6	1.7	495	9	US-10-003-392-8	645	730	9	US-09-298-523B-68	Sequence 68, Appl
573	6	1.7	497	9	US-09-896-896A-1	646	731	10	US-09-910-174A-15	Sequence 15, Appl
574	6	1.7	497	10	US-09-753-126-1	647	751	9	US-09-738-626-6525	Sequence 6525, Ap
575	6	1.7	498	10	US-09-323-998D-57	648	775	9	US-09-738-626-3773	Sequence 3773, Ap
576	6	1.7	500	9	US-10-157-855-17	649	782	10	US-09-866-582-16	Sequence 16, Appl
577	6	1.7	500	10	US-09-323-998D-58	650	783	10	US-09-864-761-38209	Sequence 38209, A
578	6	1.7	500	10	US-09-323-998D-59	651	802	10	US-09-757-049A-1	Sequence 1, Appl
579	6	1.7	502	10	US-09-323-998D-56	652	803	10	US-09-738-363-12	Sequence 12, Appl
580	6	1.7	504	10	US-09-765-205-40	653	807	10	US-09-801-368-394	Sequence 394, App
581	6	1.7	506	9	US-10-108-605-295	654	809	9	US-09-742-312-2	Sequence 2, Appl
582	6	1.7	507	10	US-09-876-187-2	655	811	9	US-10-078-770-124	Sequence 124, App
583	6	1.7	507	10	US-09-749-728B-13	656	852	9	US-09-738-626-6999	Sequence 93, Appl
584	6	1.7	522	10	US-09-815-242-11002	657	862	10	US-09-742-312-4	Sequence 4, Appl
585	6	1.7	522	12	US-10-090-624-4	658	873	10	US-09-911-824-61	Sequence 61, Appl
586	6	1.7	523	9	US-10-102-806-721	659	915	10	US-09-817-514A-6	Sequence 6, Appl
587	6	1.7	527	9	US-09-935-642-13	660	916	9	US-09-738-626-6353	Sequence 6353, Ap
588	6	1.7	531	10	US-09-833-790-255	661	923	9	US-09-820-843A-112	Sequence 112, App
589	6	1.7	533	10	US-09-815-242-11376	662	923	9	US-09-298-523B-60	Sequence 60, Appl
590	6	1.7	535	9	US-09-968-851-38	663	1012	10	US-09-876-527-16	Sequence 16, Appl
591	6	1.7	551	10	US-09-815-242-10500	664	1026	9	US-09-947-063-4	Sequence 4, Appl
592	6	1.7	552	10	US-09-824-735-4	665	1026	9	US-09-947-063-11	Sequence 11, Appl
593	6	1.7	563	10	US-09-793-848A-2	666	1026	9	US-09-947-063-12	Sequence 12, Appl
594	6	1.7	563	10	US-09-815-242-13430	667	1084	12	US-10-071-900-3	Sequence 3, Appl
595	6	1.7	565	9	US-10-081-051-35	668	1184	9	US-09-978-295A-425	Sequence 425, App
596	6	1.7	568	9	US-09-738-626-4343	669	1184	9	US-09-978-697-425	Sequence 425, App
597	6	1.7	568	9	US-09-746-660A-118	670	1184	9	US-09-978-192A-425	Sequence 425, App
598	6	1.7	584	9	US-09-806-738-18	671	1184	9	US-09-999-832A-425	Sequence 425, App
599	6	1.7	584	10	US-09-810-174A-16	672	1184	9	US-09-978-189-425	Sequence 425, App
600	6	1.7	584	10	US-09-955-866-12	673	1184	9	US-10-028-072-394	Sequence 394, App
601	6	1.7	592	10	US-09-753-126-4	674	1184	9	US-10-121-049-394	Sequence 394, App
602	6	1.7	597	9	US-09-996-634-129	675	1184	9	US-10-123-904-394	Sequence 394, App
603	6	1.7	597	9	US-09-997-181-129	676	1184	9	US-10-140-470-394	Sequence 394, App

677	6	1.7	1184	9	US-10-175-746-394	Sequence 394, App	750	6	1.7	2697	10	US-09-961-527A-5	Sequence 5, Appl1
678	6	1.7	1184	9	US-10-176-918-394	Sequence 394, App	751	6	1.7	2724	9	US-09-808-602-13	Sequence 13, Appl
679	6	1.7	1184	9	US-10-176-921-394	Sequence 394, App	752	6	1.7	2733	9	US-09-808-602-8	Sequence 8, Appl1
680	6	1.7	1184	9	US-10-137-865-394	Sequence 394, App	753	6	1.7	2764	9	US-09-808-602-80	Sequence 80, Appl
681	6	1.7	1184	9	US-10-140-474-394	Sequence 394, App	754	6	1.7	2765	9	US-09-808-602-84	Sequence 84, Appl
682	6	1.7	1184	9	US-10-142-431-394	Sequence 394, App	755	6	1.7	2802	9	US-09-808-602-81	Sequence 81, Appl
683	6	1.7	1184	9	US-10-143-114-394	Sequence 394, App	756	6	1.7	3158	10	US-09-815-242-12611	Sequence 12611, A
684	6	1.7	1184	9	US-10-140-002-394	Sequence 394, App	757	6	1.7	6281	10	US-09-815-242-12996	Sequence 12996, A
685	6	1.7	1184	9	US-09-978-608A-425	Sequence 425, App	758	6	1.7	26926	9	US-09-759-508B-2	Sequence 2, Appl1
686	6	1.7	1184	9	US-10-142-419-394	Sequence 394, App	759	5	1.5	6	10	US-09-835-087-19	Sequence 19, Appl
687	6	1.7	1184	9	US-09-978-191A-425	Sequence 425, App	760	5	1.5	8	10	US-09-770-595A-9	Sequence 9, Appl1
688	6	1.7	1184	9	US-09-978-403A-425	Sequence 425, App	761	5	1.5	8	10	US-09-844-988-21	Sequence 21, Appl
689	6	1.7	1184	9	US-09-978-564A-425	Sequence 425, App	762	5	1.5	8	10	US-09-844-908-21	Sequence 21, Appl
690	6	1.7	1184	9	US-09-978-585A-425	Sequence 425, App	763	5	1.5	9	10	US-09-779-308-191	Sequence 191, App
691	6	1.7	1184	9	US-10-017-081A-425	Sequence 425, App	764	5	1.5	10	9	US-09-017-743C-87	Sequence 87, Appl
692	6	1.7	1184	9	US-10-123-282-394	Sequence 394, App	765	5	1.5	10	9	US-09-955-732-16	Sequence 16, Appl
693	6	1.7	1184	9	US-10-142-423-394	Sequence 394, App	766	5	1.5	10	9	US-09-945-917-18	Sequence 18, Appl
694	6	1.7	1184	9	US-09-978-824-425	Sequence 425, App	767	5	1.5	10	9	US-09-955-732-16	Sequence 16, Appl
695	6	1.7	1184	9	US-09-981-915A-425	Sequence 425, App	768	5	1.5	10	10	US-09-770-595A-4	Sequence 4, Appl1
696	6	1.7	1184	9	US-09-999-833A-425	Sequence 425, App	769	5	1.5	10	10	US-09-779-308-230	Sequence 230, App
697	6	1.7	1184	9	US-10-121-050-394	Sequence 394, App	770	5	1.5	10	10	US-09-779-308-444	Sequence 444, App
698	6	1.7	1184	9	US-10-141-755-394	Sequence 394, App	771	5	1.5	11	9	US-10-033-741-23	Sequence 23, Appl
699	6	1.7	1184	9	US-10-167-749-425	Sequence 394, App	772	5	1.5	11	10	US-09-734-520-84	Sequence 84, Appl
700	6	1.7	1184	9	US-09-918-585A-425	Sequence 425, App	773	5	1.5	11	12	US-10-012-024A-84	Sequence 84, Appl
701	6	1.7	1184	9	US-10-143-032-394	Sequence 394, App	774	5	1.5	12	10	US-09-839-666-8	Sequence 8, Appl1
702	6	1.7	1187	10	US-09-768-436-4	Sequence 2, Appl1	775	5	1.5	12	10	US-09-839-666-8	Sequence 8, Appl1
703	6	1.7	1192	10	US-09-789-386-2	Sequence 2, Appl1	776	5	1.5	12	10	US-09-839-666-9	Sequence 9, Appl1
704	6	1.7	1192	10	US-09-758-140-6	Sequence 2, Appl1	777	5	1.5	12	10	US-09-770-595A-7	Sequence 7, Appl1
705	6	1.7	1192	10	US-09-833-348-23	Sequence 2, Appl1	778	5	1.5	12	10	US-09-832-723-19	Sequence 19, Appl
706	6	1.7	1192	10	US-09-833-348-23	Sequence 2, Appl1	779	5	1.5	13	9	US-09-968-436B-9	Sequence 9, Appl1
707	6	1.7	1196	9	US-09-823-394-2	Sequence 2, Appl1	780	5	1.5	13	9	US-10-044-703-34	Sequence 34, Appl
708	6	1.7	1214	9	US-09-945-901-54	Sequence 54, Appl	781	5	1.5	13	9	US-10-033-741-23	Sequence 23, Appl
709	6	1.7	1214	9	US-10-007-747-54	Sequence 54, Appl	782	5	1.5	13	10	US-09-879-936-25	Sequence 25, Appl
710	6	1.7	1214	9	US-10-038-937-54	Sequence 54, Appl	783	5	1.5	14	10	US-09-813-333-34	Sequence 34, Appl
711	6	1.7	1215	10	US-09-815-242-5908	Sequence 5908, Ap	784	5	1.5	14	9	US-10-024-123-40	Sequence 40, Appl
712	6	1.7	1219	9	US-09-945-901-50	Sequence 50, Appl	785	5	1.5	14	10	US-09-903-412-9	Sequence 9, Appl1
713	6	1.7	1219	9	US-10-007-747-50	Sequence 50, Appl	786	5	1.5	15	9	US-10-211-069-9	Sequence 9, Appl1
714	6	1.7	1219	9	US-10-038-937-50	Sequence 50, Appl	787	5	1.5	15	10	US-09-916-201-7	Sequence 7, Appl1
715	6	1.7	1231	9	US-09-945-901-48	Sequence 48, Appl	788	5	1.5	16	9	US-09-967-237-16	Sequence 16, Appl
716	6	1.7	1231	9	US-10-007-747-48	Sequence 48, Appl	789	5	1.5	16	10	US-09-772-719-16	Sequence 16, Appl
717	6	1.7	1231	9	US-10-038-937-48	Sequence 48, Appl	790	5	1.5	17	9	US-09-984-245-308	Sequence 308, App
718	6	1.7	1236	9	US-09-945-901-6	Sequence 6, Appl1	791	5	1.5	17	9	US-09-966-262-308	Sequence 308, App
719	6	1.7	1236	9	US-10-007-747-6	Sequence 6, Appl1	792	5	1.5	17	9	US-09-880-748-2862	Sequence 2862, Ap
720	6	1.7	1236	9	US-10-038-937-6	Sequence 6, Appl1	793	5	1.5	17	9	US-09-983-966-308	Sequence 308, App
721	6	1.7	1239	9	US-09-945-901-52	Sequence 52, Appl	794	5	1.5	17	9	US-09-983-966-308	Sequence 308, App
722	6	1.7	1239	9	US-10-007-747-52	Sequence 52, Appl	795	5	1.5	17	10	US-09-879-936-9	Sequence 9, Appl1
723	6	1.7	1239	9	US-10-038-937-52	Sequence 52, Appl	796	5	1.5	17	10	US-09-864-761-34508	Sequence 34508, A
724	6	1.7	1244	9	US-09-945-901-46	Sequence 46, Appl	797	5	1.5	17	10	US-09-880-713A-16	Sequence 16, Appl
725	6	1.7	1244	9	US-10-007-747-46	Sequence 46, Appl	798	5	1.5	17	10	US-09-988-842-7	Sequence 7, Appl1
726	6	1.7	1244	9	US-10-038-937-46	Sequence 46, Appl	799	5	1.5	18	10	US-09-864-761-40786	Sequence 40786, A
727	6	1.7	1247	10	US-09-815-242-10145	Sequence 10145, A	800	5	1.5	18	9	US-10-038-612-33	Sequence 33, Appl
728	6	1.7	1269	10	US-09-815-242-13113	Sequence 13113, A	801	5	1.5	19	9	US-10-038-612-33	Sequence 33, Appl
729	6	1.7	1333	10	US-09-815-242-10336	Sequence 10336, A	802	5	1.5	19	10	US-09-954-349-11	Sequence 11, Appl
730	6	1.7	1354	10	US-09-808-571A-4	Sequence 4, Appl1	803	5	1.5	20	9	US-10-038-612-151	Sequence 151, App
731	6	1.7	1447	10	US-09-808-571A-4	Sequence 2, Appl1	804	5	1.5	20	9	US-10-044-703-22	Sequence 22, Appl
732	6	1.7	1460	10	US-09-815-242-13668	Sequence 13668, A	805	5	1.5	20	10	US-09-864-761-34828	Sequence 34828, A
733	6	1.7	1464	9	US-09-945-901-11	Sequence 11, Appl	806	5	1.5	20	10	US-09-813-333-22	Sequence 22, Appl
734	6	1.7	1464	9	US-10-007-747-11	Sequence 11, Appl	807	5	1.5	21	9	US-10-124-800-15	Sequence 15, Appl
735	6	1.7	1464	9	US-10-038-937-11	Sequence 11, Appl	808	5	1.5	21	9	US-10-051-643-4	Sequence 4, Appl1
736	6	1.7	1488	9	US-09-738-626-5495	Sequence 5495, Ap	809	5	1.5	21	9	US-09-880-505-4	Sequence 4, Appl1
737	6	1.7	1504	9	US-09-932-145-7	Sequence 7, Appl1	810	5	1.5	21	9	US-09-880-505-13	Sequence 13, Appl
738	6	1.7	1723	10	US-09-841-132-394	Sequence 394, App	811	5	1.5	21	10	US-09-775-923-3	Sequence 3, Appl1
739	6	1.7	1723	10	US-09-841-132-395	Sequence 395, App	812	5	1.5	22	9	US-09-349-755-9	Sequence 9, Appl1
740	6	1.7	1802	10	US-09-965-553-18	Sequence 18, Appl	813	5	1.5	22	9	US-09-349-755-16	Sequence 16, Appl
741	6	1.7	2008	9	US-09-736-968A-105	Sequence 105, App	814	5	1.5	22	9	US-09-349-755-35	Sequence 35, Appl
742	6	1.7	2008	10	US-09-736-969A-2	Sequence 2, Appl1	815	5	1.5	22	9	US-09-166-334-9	Sequence 9, Appl1
743	6	1.7	2008	10	US-09-736-969A-91	Sequence 91, Appl	816	5	1.5	22	9	US-09-166-334-16	Sequence 16, Appl
744	6	1.7	2008	10	US-09-736-960-88	Sequence 88, Appl	817	5	1.5	22	9	US-09-166-334-35	Sequence 35, Appl
745	6	1.7	2025	10	US-09-801-242-5703	Sequence 5703, Ap	818	5	1.5	22	9	US-09-955-732-18	Sequence 18, Appl
746	6	1.7	2026	10	US-09-815-242-5703	Sequence 86, Appl	819	5	1.5	22	9	US-09-752-724-9	Sequence 9, Appl1
747	6	1.7	2120	9	US-09-801-368-86	Sequence 2, Appl1	820	5	1.5	22	10	US-09-752-724-9	Sequence 10, Appl
748	6	1.7	2437	10	US-09-815-242-5834	Sequence 5834, Ap	821	5	1.5	22	10	US-09-752-724-9	Sequence 10, Appl
749	6	1.7	2472	10	US-09-815-242-5064	Sequence 5064, Ap	822	5	1.5	22	10	US-09-752-724-9	Sequence 10, Appl

823	5	1.5	22	10	US-09-864-761-44867	Sequence 44867, A	896	5	1.5	42	10	US-09-848-664-14	Sequence 14, Appl
824	5	1.5	22	10	US-09-985-297-46	Sequence 46, Appl	897	5	1.5	43	10	US-09-864-761-47609	Sequence 47609, A
825	5	1.5	22	10	US-09-350-206-9	Sequence 9, Appl	898	5	1.5	44	10	US-09-864-761-36103	Sequence 36103, A
826	5	1.5	22	10	US-09-350-206-16	Sequence 16, Appl	899	5	1.5	44	10	US-09-864-761-42196	Sequence 42196, A
827	5	1.5	22	10	US-09-350-206-35	Sequence 35, Appl	900	5	1.5	45	10	US-09-864-761-37820	Sequence 37820, A
828	5	1.5	22	10	US-09-925-442-31	Sequence 31, Appl	901	5	1.5	45	10	US-09-864-761-37820	Sequence 37820, A
829	5	1.5	22	10	US-09-912-425-3	Sequence 3, Appl	902	5	1.5	46	9	US-10-102-806-486	Sequence 1821, Ap
830	5	1.5	23	9	US-10-097-065-451	Sequence 451, App	903	5	1.5	46	9	US-10-102-806-486	Sequence 486, App
831	5	1.5	24	10	US-09-864-761-38685	Sequence 38685, A	904	5	1.5	47	9	US-09-812-485A-4	Sequence 44815, A
832	5	1.5	25	9	US-10-051-643-20	Sequence 20, Appl	905	5	1.5	47	9	US-09-864-761-44815	Sequence 4, Appl
833	5	1.5	25	9	US-09-880-505-20	Sequence 20, Appl	906	5	1.5	48	10	US-09-939-980-299	Sequence 299, App
834	5	1.5	25	9	US-09-967-237-53	Sequence 53, Appl	907	5	1.5	48	10	US-09-864-761-43341	Sequence 43341, A
835	5	1.5	25	9	US-10-044-708A-5	Sequence 5, Appl	908	5	1.5	49	10	US-09-764-860-391	Sequence 391, App
836	5	1.5	25	10	US-09-276-600-4	Sequence 9, Appl	909	5	1.5	50	9	US-10-012-896-585	Sequence 585, App
837	5	1.5	25	10	US-09-821-984-92	Sequence 42, Appl	910	5	1.5	50	9	US-10-032-896-385	Sequence 385, App
838	5	1.5	25	10	US-09-815-108-12	Sequence 12, Appl	911	5	1.5	50	9	US-09-895-793-585	Sequence 6, Appl
839	5	1.5	25	10	US-09-864-761-38662	Sequence 38662, A	912	5	1.5	50	9	US-09-895-814-585	Sequence 585, App
840	5	1.5	25	10	US-09-864-761-45997	Sequence 45, Appl	913	5	1.5	50	9	US-10-097-065-376	Sequence 376, App
841	5	1.5	25	10	US-09-938-315-45	Sequence 45, Appl	914	5	1.5	50	10	US-09-759-143-585	Sequence 585, App
842	5	1.5	25	10	US-09-772-719-53	Sequence 53, Appl	915	5	1.5	50	10	US-09-864-761-45994	Sequence 45994, A
843	5	1.5	26	9	US-10-097-065-431	Sequence 431, App	916	5	1.5	50	10	US-09-780-669-585	Sequence 585, App
844	5	1.5	26	10	US-09-870-162A-25	Sequence 25, Appl	917	5	1.5	51	9	US-10-093-200A-5	Sequence 5, Appl
845	5	1.5	26	10	US-09-864-761-37585	Sequence 37585, A	918	5	1.5	52	9	US-09-774-639-258	Sequence 258, App
846	5	1.5	26	10	US-09-864-761-41715	Sequence 41715, A	919	5	1.5	52	9	US-09-969-730-315	Sequence 315, App
847	5	1.5	27	9	US-10-223-047-23	Sequence 23, Appl	920	5	1.5	52	9	US-10-033-357-1158	Sequence 1158, Ap
848	5	1.5	27	9	US-10-097-065-439	Sequence 439, App	921	5	1.5	52	10	US-09-864-761-37509	Sequence 37509, A
849	5	1.5	27	9	US-10-097-065-440	Sequence 440, App	922	5	1.5	53	10	US-09-864-761-33447	Sequence 33447, A
850	5	1.5	28	10	US-09-864-761-34499	Sequence 34499, A	923	5	1.5	53	10	US-09-864-761-46621	Sequence 46621, A
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852	5	1.5	29	10	US-09-729-835-95	Sequence 95, Appl	925	5	1.5	53	10	US-09-873-880-12	Sequence 12, Appl
853	5	1.5	29	10	US-09-752-724-8	Sequence 8, Appl	926	5	1.5	53	10	US-09-071-838-178	Sequence 178, App
854	5	1.5	30	10	US-09-864-761-34443	Sequence 34443, A	927	5	1.5	54	9	US-09-796-692-1101	Sequence 1101, Ap
855	5	1.5	30	10	US-09-864-761-40820	Sequence 40820, A	928	5	1.5	54	10	US-09-864-761-43048	Sequence 43048, A
856	5	1.5	30	10	US-09-864-761-45392	Sequence 45392, A	929	5	1.5	54	10	US-09-796-338A-21	Sequence 21, Appl
857	5	1.5	32	10	US-09-752-724-6	Sequence 6, Appl	930	5	1.5	54	12	US-10-016-768-3	Sequence 3, Appl
858	5	1.5	32	10	US-09-864-761-35733	Sequence 35733, A	931	5	1.5	55	10	US-09-864-761-35539	Sequence 35539, A
859	5	1.5	32	10	US-09-864-761-46491	Sequence 46491, A	932	5	1.5	55	12	US-10-001-879-172	Sequence 172, App
860	5	1.5	33	10	US-09-737-379-7	Sequence 7, Appl	933	5	1.5	56	9	US-09-902-941-1885	Sequence 1885, Ap
861	5	1.5	33	10	US-09-864-761-46125	Sequence 46125, A	934	5	1.5	56	9	US-09-796-692-2432	Sequence 2432, Ap
862	5	1.5	33	10	US-09-864-761-46457	Sequence 46457, A	935	5	1.5	56	9	US-09-849-826-1885	Sequence 1885, Ap
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864	5	1.5	34	10	US-09-864-761-36562	Sequence 36562, A	937	5	1.5	56	10	US-09-864-761-44380	Sequence 44380, A
865	5	1.5	34	10	US-09-864-761-45967	Sequence 45967, A	938	5	1.5	56	10	US-09-864-761-48411	Sequence 48411, A
866	5	1.5	35	10	US-09-864-761-38264	Sequence 38264, A	939	5	1.5	57	9	US-09-989-920-227	Sequence 227, App
867	5	1.5	36	9	US-09-809-391-736	Sequence 736, App	940	5	1.5	57	9	US-09-874-056-3	Sequence 3, Appl
868	5	1.5	37	9	US-09-967-237-6	Sequence 7, Appl	941	5	1.5	57	9	US-09-874-056-4	Sequence 4, Appl
869	5	1.5	37	9	US-10-196-703-7	Sequence 34, Appl	942	5	1.5	57	9	US-10-091-504-898	Sequence 898, App
870	5	1.5	37	9	US-10-196-703-24	Sequence 34, Appl	943	5	1.5	57	10	US-09-864-761-37634	Sequence 37634, A
871	5	1.5	37	9	US-10-196-703-35	Sequence 35, Appl	944	5	1.5	57	10	US-09-764-869-898	Sequence 898, App
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873	5	1.5	37	9	US-10-196-703-37	Sequence 37, Appl	946	5	1.5	58	9	US-09-874-056-5	Sequence 5, Appl
874	5	1.5	37	10	US-09-772-719-6	Sequence 6, Appl	947	5	1.5	58	9	US-09-874-056-7	Sequence 7, Appl
875	5	1.5	38	10	US-09-864-761-36955	Sequence 36955, A	948	5	1.5	58	9	US-10-016-157A-172	Sequence 172, App
876	5	1.5	38	10	US-09-864-761-44495	Sequence 44495, A	949	5	1.5	58	9	US-10-116-235-37	Sequence 37, Appl
877	5	1.5	38	10	US-09-864-761-46302	Sequence 44302, A	950	5	1.5	58	10	US-09-739-254-98	Sequence 98, Appl
878	5	1.5	39	9	US-09-843-676-23	Sequence 23, Appl	951	5	1.5	58	10	US-09-904-615-98	Sequence 98, Appl
879	5	1.5	39	9	US-09-766-253-23	Sequence 23, Appl	952	5	1.5	58	10	US-09-864-761-34517	Sequence 34517, A
880	5	1.5	39	9	US-09-438-486-23	Sequence 23, Appl	953	5	1.5	58	10	US-09-867-852-96	Sequence 96, Appl
881	5	1.5	39	9	US-10-053-758-23	Sequence 23, Appl	954	5	1.5	59	9	US-09-874-056-6	Sequence 6, Appl
882	5	1.5	39	9	US-10-054-295-23	Sequence 23, Appl	955	5	1.5	59	10	US-09-864-761-41455	Sequence 41455, A
883	5	1.5	39	9	US-10-054-611-33	Sequence 23, Appl	956	5	1.5	59	10	US-09-864-761-1381	Sequence 1381, Ap
884	5	1.5	39	10	US-09-864-761-39503	Sequence 39503, A	957	5	1.5	59	10	US-09-895-913A-192	Sequence 192, App
885	5	1.5	40	9	US-10-083-357-1053	Sequence 1053, Ap	958	5	1.5	60	9	US-10-012-896-586	Sequence 586, App
886	5	1.5	41	10	US-09-864-761-36039	Sequence 36039, A	959	5	1.5	60	9	US-10-012-896-886	Sequence 886, App
887	5	1.5	41	9	US-09-922-199A-13	Sequence 13, Appl	960	5	1.5	60	9	US-10-012-896-892	Sequence 892, App
888	5	1.5	41	9	US-09-948-820-47	Sequence 47, Appl	961	5	1.5	60	9	US-09-895-793-586	Sequence 586, App
889	5	1.5	41	10	US-09-864-761-40165	Sequence 40165, A	962	5	1.5	60	9	US-09-895-793-886	Sequence 886, App
890	5	1.5	41	10	US-09-864-761-45355	Sequence 45355, A	963	5	1.5	60	9	US-09-895-793-892	Sequence 892, App
891	5	1.5	42	10	US-09-870-162A-24	Sequence 24, Appl	964	5	1.5	60	9	US-09-895-814-586	Sequence 586, App
892	5	1.5	42	10	US-09-864-761-46961	Sequence 46961, A	965	5	1.5	60	9	US-09-895-814-886	Sequence 886, App
893	5	1.5	42	10	US-09-764-860-492	Sequence 492, App	966	5	1.5	60	9	US-09-895-814-892	Sequence 892, App
894	5	1.5	42	10	US-09-848-664-12	Sequence 12, Appl	967	5	1.5	60	10	US-09-759-143-586	Sequence 586, App
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Query Match      2.3%; Score 8; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 PAPAPAPE 207
Db 2 PAPAPAPE 9

RESULT 4
US-09-864-761-38830
; Sequence 38830, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38830
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO 283844.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.7
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; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
; OTHER INFORMATION: SWISSPROT HIT: P55194, EVALUAE 3.10e-01
US-09-864-761-38830
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Best Local Similarity 100.0%; Pred. No. 2.4;
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QY 199 APAPAPAP 206
Db 40 APAPAPAP 47
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RESULT 5
US-09-922-199A-14
; Sequence 14, Application US/09922199A
; Publication No. US20020187138A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 15368, A NOVEL HUMAN GTP-RELEASING
; FILE REFERENCE: 381552002500
; CURRENT APPLICATION NUMBER: US/09/922,199A
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/222,622
; PRIOR FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 14
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-09-922-199A-14
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Best Local Similarity 100.0%; Pred. No. 2.6;
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QY 200 PAPAPAPE 207
Db 2 PAPAPAPE 9
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RESULT 6
US-09-738-626-3880
; Sequence 3880, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
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; SOFTWARE: PatentIn ver. 3.0

; SEQ ID NO 3880

; LENGTH: 191

; TYPE: PRT

; ORGANISM: Corynebacterium glutamicum

US-09-738-626-3880

Query Match

; Sequence 54, Application US/09965703

; Best Local Similarity 100.0%; Pred. No. 6.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAPAP 206

Db 115 APAPAPAP 122

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RESULT 7

US-09-965-703-54

; Sequence 54, Application US/09965703

; Patent No. US20020119521A1

; GENERAL INFORMATION:

; APPLICANT: Rohm and Haas Company

; APPLICANT: Palli, Subba Reddy

; APPLICANT: Kapitskaya, Marianna Zinovjevna

; APPLICANT: Cress, Dean Ervin

; TITLE OF INVENTION: No. US20020119521A1el Ecdysone Receptor-Based Inducible Gene Expr

; FILE REFERENCE: A010208

; CURRENT APPLICATION NUMBER: US/09/965,703

; CURRENT FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: 60/191,355

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 60/269,799

; PRIOR FILING DATE: 2001-02-20

; PRIOR APPLICATION NUMBER: PCT/US01/09050

; PRIOR FILING DATE: 2001-03-21

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 54

; LENGTH: 269

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-965-703-54

Query Match

; Sequence 50, Application US/10042417

; Best Local Similarity 100.0%; Pred. No. 9.1;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAPAP 206

Db 108 APAPAPAP 115

|||||

RESULT 8

US-10-042-417-50

; Sequence 50, Application US/10042417

; Patent No. US20020123082A1

; GENERAL INFORMATION:

; APPLICANT: pagano, M.

; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF

; PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS

; FILE REFERENCE: 5914-090-999

; CURRENT APPLICATION NUMBER: US/10/042,417

; CURRENT FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: 60/260,179

; PRIOR FILING DATE: 2001-01-5

; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 50

; LENGTH: 283

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-042-417-50

Query Match

; Sequence 1040, Application US/09764868

; Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAPAP 206

Db 3 APAPAPAP 10

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RESULT 9

US-09-764-868-1040

; Sequence 1040, Application US/09764868

; Patent No. US20020168711A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PR232

; CURRENT APPLICATION NUMBER: US/09/764,868

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 1510

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1040

; LENGTH: 332

; TYPE: PRT

; ORGANISM: Homo sapiens

; NAME/KEY: SITE

; LOCATION: (72)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (81)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (89)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (91)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (106)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (270)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (275)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (280)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (283)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (307)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (313)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (321)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (329)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (329)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (329)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

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Db 261 APAPAPAP 268

RESULT 10
US-09-291-417-6
; Sequence 6, Application US/09291417A
; Publication No. US20030050230A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 240/300
; CURRENT APPLICATION NUMBER: US/09/291,417A
; EARLIER FILING DATE: 1999-04-13
; EARLIER FILING DATE: 1999-04-13
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Mammalian (Human) STLK3
US-09-291-417-6

Query Match 2.3%; Score 8; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAPAP 206
Db 11 APAPAPAP 18

RESULT 11
US-09-771-161A-272
; Sequence 272, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR FILING DATE: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 272
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-272

Query Match 2.3%; Score 8; DB 10; Length 547;
Best Local Similarity 100.0%; Pred. No. 17;
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QY 199 APAPAPAP 206
Db 42 APAPAPAP 49

RESULT 12
US-09-771-161A-273
; Sequence 273, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: BRILES et al.
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
; FILE REFERENCE: 454312-3140
; CURRENT APPLICATION NUMBER: US/09/298,523B
; CURRENT FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 62
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae

QY 200 PAPAPAPE 207
Db 615 PAPAPAPE 622

RESULT 14
US-09-298-523B-62
; Sequence 62, Application US/09298523B
; Publication No. US20030059438A1
; GENERAL INFORMATION:
; APPLICANT: BRILES et al.
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
; FILE REFERENCE: 454312-3140
; CURRENT APPLICATION NUMBER: US/09/298,523B
; CURRENT FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 62
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae

QY 200 PAPAPAPE 207
Db 615 PAPAPAPE 622

RESULT 13
US-09-298-523B-63
; Sequence 63, Application US/09298523B
; Publication No. US20030059438A1
; GENERAL INFORMATION:
; APPLICANT: BRILES et al.
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
; FILE REFERENCE: 454312-3140
; CURRENT APPLICATION NUMBER: US/09/298,523B
; CURRENT FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-298-523B-63

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Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 42 APAPAPAP 49

RESULT 13
US-09-298-523B-63
; Sequence 63, Application US/09298523B
; Publication No. US20030059438A1
; GENERAL INFORMATION:
; APPLICANT: BRILES et al.
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
; FILE REFERENCE: 454312-3140
; CURRENT APPLICATION NUMBER: US/09/298,523B
; CURRENT FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-298-523B-63

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Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 PAPAPAPE 207
Db 615 PAPAPAPE 622

RESULT 14
US-09-298-523B-62
; Sequence 62, Application US/09298523B
; Publication No. US20030059438A1
; GENERAL INFORMATION:
; APPLICANT: BRILES et al.
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
; FILE REFERENCE: 454312-3140
; CURRENT APPLICATION NUMBER: US/09/298,523B
; CURRENT FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 62
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae

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Db 615 PAPAPAPE 622
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US-09-298-523B-62

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Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 646 PAPAPAPE 653

RESULT 15

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; Sequence 2; Application US/09298523B
; Publication No. US20030059438A1
; GENERAL INFORMATION:
; APPLICANT: BRILES et al.
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
; FILE REFERENCE: 454312-3140
; CURRENT APPLICATION NUMBER: US/09/298,523B
; CURRENT FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-298-523B-2

Query Match 2.3%; Score 8; DB 9; Length 707;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 200 PAPAPAPE 207
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Job time : 38 secs

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OM protein - protein search, using sw model

Run on: April 15, 2003, 08:53:24 ; Search time 18 Seconds
(without alignments):
1837.236 Million cell updates/sec

Title: US-09-831-061-2

Perfect score: 344

Sequence: 1 MKAIFVLNAAPKDNWYAGG.....DRRVEIEVKGKVEVTPAG 344

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Gapop 60.0 , Gapext 60.0

Searched: 283224 segs, 96134422 residues

Word size : 5

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

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1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	53	15.4	238	2	outer membrane pro
3	53	15.4	350	2	outer membrane pro
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5	33	9.6	346	1	MNECA
6	33	9.6	346	2	outer membrane pro
7	33	9.6	346	2	outer membrane pro
8	29	8.4	243	2	outer membrane pro
9	29	8.4	243	2	outer membrane pro
10	29	8.4	244	2	outer membrane pro
11	27	7.8	243	2	outer membrane pro
12	27	7.8	243	2	outer membrane pro
13	24	7.0	351	1	MNEBAC
14	22	6.4	350	1	MNEBAC
15	22	6.4	350	2	outer membrane pro
16	22	6.4	353	2	outer membrane pro
17	20	5.8	240	2	outer membrane pro
18	20	5.8	241	2	outer membrane pro
19	20	5.8	241	2	outer membrane pro
20	19	5.5	359	2	outer membrane pro
21	12	3.5	349	2	outer membrane pro
22	9	2.6	187	2	outer membrane pro
23	9	2.6	193	1	MORT4E
24	9	2.6	197	1	MOHU4E
25	9	2.6	215	2	S55925
26	9	2.6	383	2	A43470
27	9	2.6	458	2	H82051
28	9	2.6	581	2	T22341
29	9	2.6	1061	1	S27311

30	1061	2	F90811	RNase E [imported]
31	1061	2	B85671	RNase E [similarit
32	1785	2	A45546	major merzotite su
33	1895	2	T15881	hypothetical prote
34	2.6	2	A48205	All-1 protein +GPE
35	28	2	A60752	outer membrane pro
36	2.3	2	B27191	nonhistone chromos
37	84	2	T23177	hypothetical prote
38	2.3	2	C90744	hypothetical prote
39	2.3	2	G85594	hypothetical prote
40	2.3	2	D46822	YbjH protein, precu
41	129	2	D49094	methymalonyl-CoA
42	134	2	T44984	hypothetical prote
43	145	2	T33037	hypothetical prote
44	163	2	D87519	glcG protein, prob
45	165	2	S35195	hypothetical prote
46	182	2	C87097	conserved hypotet
47	188	2	A23253	myosin A1 catalyti
48	189	2	I57590	myosin light chain
49	190	2	MORT4E	myosin alkali high
50	190	2	T25462	hypothetical prote
51	192	1	MORBLA	myosin alkali high
52	192	1	MOCHLA	myosin alkali high
53	208	2	A87269	hypothetical prote
54	2.3	2	D87312	hypothetical prote
55	2.3	2	G70555	conserved hypotet
56	2.3	2	B75318	hypothetical prote
57	2.3	2	T51206	ferripyochelin-bin
58	2.3	2	S07264	beta-crystallin B1
59	2.3	2	D84461	hypothetical prote
60	2.3	2	JN0747	histone H1-I - Vol
61	2.3	2	RBSMHP	mammosyl-glycoprot
62	313	1	G02424	cyclin-dependent k
63	316	2	B40951	TiF1 protein - mou
64	331	2	S46745	hypothetical prote
65	344	2	T46916	hypothetical prote
66	346	2	C64187	outer membrane pro
67	353	2	T30402	hypothetical prote
68	361	2	T14337	RAD23 protein, iso
69	379	2	E91220	uroporphyrinogen I
70	399	2	G86066	uroporphyrinogen I
71	399	2	SKLALG	dermal gland prote
72	416	1	T51238	hypothetical elonga
73	424	2	I51238	translation elonga
74	437	2	G87675	arylesterase-relat
75	438	2	C75341	tetrapeptide
76	500	2	I53719	NF-kappa-B transcr
77	537	2	A43017	transcription fact
78	551	2	A40851	transforming prote
79	551	2	T08148	proline-rich myros
80	552	2	B55514	dihydrolipoamide S
81	553	2	H87316	hypothetical prote
82	582	2	H87304	hypothetical prote
83	584	2	T35297	probable dihydrol
84	590	1	A28088	oxaloacetate decar
85	596	2	F75302	ATP-dependent DNA
86	596	2	C82221	transport protein
87	600	2	C82221	hypothetical prote
88	642	2	EDBE22	immediate-early pr
89	676	1	EDBE22	immediate-early pr
90	676	1	EDBE22	probable tpr prote
91	676	1	EDBE22	hypothetical prote
92	693	2	G71302	hypothetical prote
93	698	2	T51915	hypothetical prote
94	747	2	T23607	hypothetical prote
95	963	2	T40290	hypothetical prote
96	1023	2	B59430	KIAA0189 protein [
97	1051	2	S55259	TiF1 protein - mou
98	1097	2	T31504	hypothetical prote
99	1151	2	T18535	high molecular mas
100	1174	2	T49868	related to suppres
101	1385	2	T14158	neurexin IV - mous
102	1513	2	T23681	hypothetical prote

103	8	2.3	1584	2	T22674	hypothetical prote	176	7	2.0	428	2	A95018	DNA-binding respon
104	8	2.3	1585	2	T31611	hypothetical prote	177	7	2.0	428	2	B97891	response regulator
105	8	2.3	2197	2	B71600	variant-specific s	178	7	2.0	430	2	AG2256	dihydrolipeamide s
106	8	2.3	2774	2	A43359	microtubule-associ	179	7	2.0	435	2	T05452	hypothetical prote
107	7	2.0	14	1	LFECW	trp operon leader	180	7	2.0	449	2	J01438	polyprotein - culi
108	7	2.0	14	2	E90858	trp operon leader	181	7	2.0	453	2	S39866	outer membrane pro
109	7	2.0	14	2	A58503	kidney and bladder	182	7	2.0	455	2	A87913	protein B0205.10 [
110	7	2.0	14	2	B85761	trp operon leader	183	7	2.0	457	2	C65203	argininosuccinate
111	7	2.0	66	2	D31844	hypothetical 7.7K	184	7	2.0	457	2	A98240	argininosuccinate
112	7	2.0	66	2	H16313	metallothionein ol	185	7	2.0	457	2	F86087	argininosuccinate
113	7	2.0	105	2	H71635	hypothetical prote	186	7	2.0	457	2	A10477	probable argininos
114	7	2.0	108	2	C72451	hypothetical prote	187	7	2.0	457	2	A95194	cell division prot
115	7	2.0	120	2	AF1646	hypothetical prote	188	7	2.0	457	2	F98060	cell division prot
116	7	2.0	125	2	S34435	protein-tyrosine k	189	7	2.0	457	2	JQ2184	hypothetical 50.4K
117	7	2.0	129	2	S65803	transcription acti	190	7	2.0	458	2	AH0935	argininosuccinate
118	7	2.0	132	2	T50779	copper chaperone h	191	7	2.0	474	2	T38485	centromere/microtu
119	7	2.0	138	2	S52933	major allergen Par	192	7	2.0	478	2	JC4940	synapsin IIB - hum
120	7	2.0	155	2	E64105	acetyl-CoA carboxy	193	7	2.0	486	2	T35445	probable integral
121	7	2.0	171	2	B96548	probable proline-r	194	7	2.0	493	2	B48362	transcription init
122	7	2.0	200	1	A71127	hypothetical prote	195	7	2.0	507	2	S05342	hypothetical prote
123	7	2.0	207	2	C84631	nodulin-like prote	196	7	2.0	515	2	S39731	pyrroline-5 carbox
124	7	2.0	208	2	A43696	Spec3 protein - se	197	7	2.0	524	2	A75588	probable protein k
125	7	2.0	210	2	AG0534	hypothetical prote	198	7	2.0	527	1	S25481	heat shock transcr
126	7	2.0	212	2	H75317	translation initia	199	7	2.0	528	2	D46449	hypothetical prote
127	7	2.0	212	2	T47918	probable DNA-bindi	200	7	2.0	551	2	F83015	hypothetical prote
128	7	2.0	213	2	T03931	DNA binding protei	201	7	2.0	556	2	D70940	probable PPE prote
129	7	2.0	222	2	H96711	hypothetical prote	202	7	2.0	568	2	F75502	threonine ammonia-
130	7	2.0	223	2	F71439	probable serine pr	203	7	2.0	574	2	F75356	serine/threonine p
131	7	2.0	228	2	S46965	microfilament shea	204	7	2.0	574	2	T43556	Wiskott-Aldrich sy
132	7	2.0	236	2	AH1630	B. subtilis late c	205	7	2.0	574	2	T38819	Wiskott-Aldrich sy
133	7	2.0	238	2	S66358	DNA-binding protei	206	7	2.0	586	2	S65802	transcription acti
134	7	2.0	246	2	T48338	arabinogalactan pr	207	7	2.0	587	2	B83015	arganyl-tRNA synth
135	7	2.0	252	2	T04739	hypothetical prote	208	7	2.0	587	2	E87420	poly-beta-hydroxyb
136	7	2.0	256	2	T10376	hypothetical prote	209	7	2.0	587	2	E85429	hypothetical prote
137	7	2.0	261	2	B81823	Deda-family integr	210	7	2.0	594	1	D55514	dihydrolipeamide d
138	7	2.0	262	2	B75365	hypothetical prote	211	7	2.0	595	2	T49384	related to NR01 pr
139	7	2.0	265	2	AG2084	ABC transporter, A	212	7	2.0	606	2	T51880	hypothetical prote
140	7	2.0	265	2	D97632	hypothetical prote	213	7	2.0	632	2	S42629	keratin K3 - rabbi
141	7	2.0	265	2	AG2855	conserved hypotet	214	7	2.0	639	2	C98264	5'-nucleotidase pr
142	7	2.0	279	2	C96721	hypothetical prote	215	7	2.0	636	2	AF3020	5'-nucleotidase [1
143	7	2.0	289	2	S56287	hypothetical prote	216	7	2.0	640	2	G70573	probable transmemb
144	7	2.0	289	2	T03395	probable lipase -	217	7	2.0	643	2	T23453	hypothetical prote
145	7	2.0	296	2	T46619	hypothetical prote	218	7	2.0	648	2	C69423	DNA helicase homol
146	7	2.0	297	2	S23737	proline-rich prote	219	7	2.0	691	2	T15983	hypothetical prote
147	7	2.0	307	2	D97605	proteinase chain h	220	7	2.0	700	2	B82788	metallopeptidase x
148	7	2.0	307	2	AF2827	HFLLC protein limpo	221	7	2.0	703	2	D81365	carbon starvation
149	7	2.0	311	2	H70511	hypothetical prote	222	7	2.0	729	2	E70803	hypothetical prote
150	7	2.0	321	2	F82104	outer membrane pro	223	7	2.0	757	2	A99561	conserved hypotet
151	7	2.0	325	2	D70666	probable modb prot	224	7	2.0	766	1	S61694	flocculation suppr
152	7	2.0	328	2	T37734	SUR4 family protei	225	7	2.0	790	1	FOVW42	gag-kit polyprotei
153	7	2.0	339	2	A37864	SCIL protein homolo	226	7	2.0	799	2	T48889	serine/threonine p
154	7	2.0	331	2	A36358	T-cell acute lymph	227	7	2.0	801	2	T29018	hypothetical prote
155	7	2.0	337	2	S55932	NCA3 protein precu	228	7	2.0	809	2	A57283	integrin beta chal
156	7	2.0	345	2	S12788	transcription fact	229	7	2.0	811	2	T36581	probable transmemb
157	7	2.0	347	2	H75253	hypothetical prote	230	7	2.0	815	2	B56708	extracellular sign
158	7	2.0	348	2	D75357	hypothetical prote	231	7	2.0	833	2	AF2089	hypothetical prote
159	7	2.0	351	1	VCNVP1	major capsid prote	232	7	2.0	852	2	S28415	guanine nucleotide
160	7	2.0	351	2	T10359	p39 capsid protei	233	7	2.0	873	2	A47283	calpottin - fruit
161	7	2.0	354	2	AB0842	glycine betaine/L-	234	7	2.0	892	2	H71558	probable translati
162	7	2.0	356	2	A13648	flagellar biosynth	235	7	2.0	907	2	AB1885	hypothetical prote
163	7	2.0	362	2	JU0353	hypothetical 39.7K	236	7	2.0	913	2	B97369	translation initia
164	7	2.0	362	2	T45072	erythroid kruppel-	237	7	2.0	913	2	AB2587	translation initia
165	7	2.0	365	2	B75398	hypothetical prote	238	7	2.0	932	2	T25941	hypothetical prote
166	7	2.0	366	2	B84712	probable protean k	239	7	2.0	930	2	B44766	defective chorion-
167	7	2.0	375	2	F75467	probable lipoprote	240	7	2.0	934	2	I51703	c-kit-related kina
168	7	2.0	379	2	T40384	probable methionin	241	7	2.0	960	1	JN0677	protein-tyrosine k
169	7	2.0	388	2	T35170	hypothetical prote	242	7	2.0	972	1	TVHUMD	macrophage colony-
170	7	2.0	407	2	A85191	probable serine pr	243	7	2.0	975	1	TVMSKT	protein-tyrosine k
171	7	2.0	407	2	B83143	probable hydrolase	244	7	2.0	975	2	T30816	macrophage colony-
172	7	2.0	413	2	JC2135	chitinase [EC 3.2.	245	7	2.0	976	1	TVMSMD	macrophage colony-
173	7	2.0	425	2	D84298	histidinol dehydro	246	7	2.0	976	1	TVHUKT	protein-tyrosine k
174	7	2.0	426	2	E97445	nitrate transport	247	7	2.0	977	2	I45877	protein-tyrosine k
175	7	2.0	426	2	AF2663	hypothetical prote	248	7	2.0	978	1	A49814	protein-tyrosine k

249	7	2.0	978	2	S16385	macrophage colony-	322	1.7	122	2	I38081	gene p27 protein -
250	7	2.0	980	1	TVCTMD	macrophage colony-	323	1.7	123	2	AD0039	diacylglycerol kin
251	7	2.0	995	2	T32466.	hypothetical prote	324	1.7	123	2	B69351	hypothetical prote
252	7	2.0	1016	2	H71460.	probable outer mem	325	1.7	124	2	C82805	DNA-binding protei
253	7	2.0	1087	2	T30844	serine-repeat anti	326	1.7	125	2	G75265	probable protein t
254	7	2.0	1095	1	A31225	phospholipase C (E	327	1.7	128	2	A29349	hypothetical prote
255	7	2.0	1111	2	T29070	hypothetical prote	328	1.7	129	2	AG2003	hypothetical prote
256	7	2.0	1123	2	A44766	defective chorion-	329	1.7	130	2	A71530	ribosomal protein
257	7	2.0	1125	1	F70177	transcription-repa	330	1.7	130	2	H81584	ribosomal protein
258	7	2.0	1131	2	S22266	FUN30 protein - ye	331	1.7	130	2	F70585	probable furB prot
259	7	2.0	1132	2	C75259	probable iron-sulf	332	1.7	130	2	S65804	transcription acti
260	7	2.0	1147	1	MWAX1B	myosin heavy chain	333	1.7	131	2	A84613	hypothetical prote
261	7	2.0	1149	2	T27567	hypothetical prote	334	1.7	132	2	T11239	hypothetical prote
262	7	2.0	1239	1	Q0BE10	BOLFI protein - hu	335	1.7	133	2	T42978	hypothetical prote
263	7	2.0	1274	2	S55050	cardiac myosin-bin	336	1.7	136	2	S74785	hypothetical prote
264	7	2.0	1298	2	A48929	protein-tyrosine k	337	1.7	137	2	T03491	conserved hypochet
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266	7	2.0	1374	2	S70712	protein-tyrosine k	339	1.7	139	2	H70784	PTS mannose-specif
267	7	2.0	1464	2	S58984	development-early pr	340	1.7	140	2	S74072	hypothetical prote
268	7	2.0	1487	1	EDBE81	immediate-early pr	341	1.7	141	2	D82745	hypothetical prote
269	7	2.0	1589	2	EDBE66	155K transcription	342	1.7	142	2	B69515	hypothetical prote
270	7	2.0	1589	2	C44766	defective chorion-	343	1.7	142	2	B69515	hypothetical prote
271	7	2.0	1618	2	S21434	nestin - human	344	1.7	147	2	T31442	probable cytochrom
272	7	2.0	2156	1	RRVUNE	genome polyprotein	345	1.7	149	2	E83633	hypothetical prote
273	7	2.0	2408	2	T24483	hypothetical prote	346	1.7	151	2	AE3643	adhesin a1a-1 (im
274	7	2.0	2649	2	T51023	hypothetical prote	347	1.7	153	2	A87400	conserved hypochet
275	6	1.7	35	2	H81948	hypothetical prote	348	1.7	154	2	S64076	probable membrane
276	6	1.7	38	1	HSPV5	histone H5 - pigeo	349	1.7	155	2	B82783	hypothetical prote
277	6	1.7	40	2	S77777	hypothetical prote	350	1.7	156	2	B87509	hypothetical prote
278	6	1.7	46	2	S07073	arabinogalactan pr	351	1.7	158	2	AI2377	conserved hypochet
279	6	1.7	48	2	AD2809	hypothetical prote	352	1.7	158	2	T02973	lipoprotein signal
280	6	1.7	67	2	B83792	small acid-soluble	353	1.7	158	2	B71096	probenazole-induce
281	6	1.7	68	2	B84050	small acid-soluble	354	1.7	158	2	D75069	hypothetical prote
282	6	1.7	70	2	T31845	hypothetical prote	355	1.7	159	2	F72754	hypothetical prote
283	6	1.7	72	1	C48380	hypothetical prote	356	1.7	161	2	S78002	hypothetical prote
284	6	1.7	73	2	E84901	small acid-soluble	357	1.7	162	2	C81808	cuticle structural
285	6	1.7	73	2	B82540	hypothetical prote	358	1.7	163	2	C91092	hypothetical prote
286	6	1.7	74	2	G82810	hypothetical prote	359	1.7	163	2	B85937	hypothetical prote
287	6	1.7	74	2	G81270	probable periplasm	360	1.7	164	2	B82800	hypothetical prote
288	6	1.7	75	2	T26916	hypothetical prote	361	1.7	165	2	A90169	hypothetical prote
289	6	1.7	79	2	AG3427	transposase BME14	362	1.7	166	2	G85057	hypothetical prote
290	6	1.7	82	2	F81521	conserved hypochet	363	1.7	167	2	B43871	probable transposa
291	6	1.7	82	2	F75326	phosphocARRIER Pro	364	1.7	168	2	JC5192	hypothetical prote
292	6	1.7	86	2	F97124	cuticle protein Lm	365	1.7	168	2	T34804	hypothetical prote
293	6	1.7	88	2	S38267	hypothetical prote	366	1.7	168	2	AE0055	hypothetical prote
294	6	1.7	89	2	A84450	hypothetical prote	367	1.7	169	2	T04162	probable lipoprote
295	6	1.7	90	2	A96505	probable glycine-r	368	1.7	169	2	E95005	hemoglobin 2 - ric
296	6	1.7	90	2	G82452	conserved hypochet	369	1.7	169	2	B97878	van2 protein, prob
297	6	1.7	92	1	WMNVPM	protein p10 - Orgy	370	1.7	170	2	G70638	telocoplanin resist
298	6	1.7	92	2	T10402	hypothetical prote	371	1.7	172	2	S62167	hypothetical prote
299	6	1.7	94	2	AG0556	phosphoenolpyruvat	372	1.7	173	2	S44407	NADH2 dehydrogenas
300	6	1.7	95	2	T34569	hypothetical prote	373	1.7	173	2	S44398	NADH2 dehydrogenas
301	6	1.7	100	2	T17126	hypothetical prote	374	1.7	173	2	S44398	NADH2 dehydrogenas
302	6	1.7	104	2	AI2257	hypothetical prote	375	1.7	173	2	S44413	NADH2 dehydrogenas
303	6	1.7	104	2	E86263	F13K23.22 protein	376	1.7	173	2	S44414	NADH2 dehydrogenas
304	6	1.7	108	2	D86877	hypothetical prote	377	1.7	173	2	S44396	NADH2 dehydrogenas
305	6	1.7	108	2	B99918	hypothetical prote	378	1.7	173	2	S44396	NADH2 dehydrogenas
306	6	1.7	109	2	G69276	conserved hypochet	379	1.7	173	2	S44412	NADH2 dehydrogenas
307	6	1.7	113	2	S77123	ribosomal protein	380	1.7	173	2	S44412	NADH2 dehydrogenas
308	6	1.7	115	2	JQ1885	V2 protein - tomat	381	1.7	173	2	S44409	NADH2 dehydrogenas
309	6	1.7	115	2	AF1044	periplasmic divale	382	1.7	173	2	S44400	NADH2 dehydrogenas
310	6	1.7	118	1	R7MCML	ribosomal protein	383	1.7	173	2	S44400	NADH2 dehydrogenas
311	6	1.7	118	2	B90259	hypothetical prote	384	1.7	173	2	S44402	NADH2 dehydrogenas
312	6	1.7	118	2	AB0282	hypothetical prote	385	1.7	173	2	S44406	NADH2 dehydrogenas
313	6	1.7	119	2	A85654	probable diacygly	386	1.7	173	2	S44411	NADH2 dehydrogenas
314	6	1.7	119	2	D90793	probable diacygly	387	1.7	173	2	S34633	NADH2 dehydrogenas
315	6	1.7	120	2	C75563	hypothetical prote	388	1.7	173	2	E90613	NADH dehydrogenase
316	6	1.7	121	2	S65793	catalase (EC 1.11.	389	1.7	173	2	E90615	NADH dehydrogenase
317	6	1.7	121	2	D86468	hypothetical prote	390	1.7	173	2	E90621	NADH dehydrogenase
318	6	1.7	122	1	KIECDG	probable diacygly	391	1.7	173	2	E90625	NADH dehydrogenase
319	6	1.7	122	2	AG1257	diacylglycerol kin	392	1.7	173	2	T11531	NADH2 dehydrogenas
320	6	1.7	122	2	AC1015	diacylglycerol kin	393	1.7	173	2	T11034	NADH2 dehydrogenas
321	6	1.7	122	2	E86097	diacylglycerol kin	394	1.7	174	2	H90003	ATP synthase B cha
												NADH dehydrogenase

gene p27 protein -
diacylglycerol kin
hypothetical prote
DNA-binding protei
probable protein t
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hypothetical prote
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hypothetical prote
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ATP synthase B cha
NADH dehydrogenase

395	6	1.7	174	2	E97240	peptidyl-prolyl ci	468	1.7	222	2	A75406	hydrolase - Deino
396	6	1.7	174	2	E65046	hypothetical prote	469	1.7	222	2	A99864	phage shock protei
397	6	1.7	175	2	T11179	NADH2 dehydrogenas	470	1.7	222	2	H82169	phage shock protei
398	6	1.7	175	2	A37786	pituitary adenylat	471	1.7	222	2	AF0658	phage shock protei
399	6	1.7	175	2	E72496	hypothetical prote	472	1.7	222	2	H85754	phage shock protei
400	6	1.7	178	2	G95090	conserved hypothet	473	1.7	222	2	C64879	phage shock protei
401	6	1.7	178	2	C97958	biotin synthase (E	474	1.7	223	2	H87335	conserved hypothet
402	6	1.7	179	2	S30994	gene 49 protein -	475	1.7	223	2	C82230	probable lipoprote
403	6	1.7	183	2	T51910	hypothetical prote	476	1.7	223	2	E89567	protein TOR9A9.9 [
404	6	1.7	183	2	C90212	conserved hypothet	477	1.7	224	2	B72040	coenzyme pqq synth
405	6	1.7	186	2	C41132	collagen-related p	478	1.7	224	2	B72040	cr610 hypothetical
406	6	1.7	187	2	S24992	photosystem II pro	479	1.7	226	2	T19891	2-haloacid dehalog
407	6	1.7	188	2	T31526	hypothetical prote	480	1.7	227	2	A38452	extensin-like prot
408	6	1.7	189	2	T36207	probable alanine-r	481	1.7	228	2	S53504	hypothetical prote
409	6	1.7	191	2	JQ1919	hypothetical prote	482	1.7	228	2	T20777	probable ABC trans
410	6	1.7	192	2	A56141	hypothetical 21.3K	483	1.7	230	2	D75518	oxidase [imported]
411	6	1.7	192	2	A12271	ribonuclease H (BC	484	1.7	230	2	E72470	hypothetical prote
412	6	1.7	193	1	HSG55	histone H5 - goose	485	1.7	230	2	AB2068	cuticular protein
413	6	1.7	193	2	H83722	transcription regu	486	1.7	230	2	AB2068	transforming prote
414	6	1.7	194	1	HSTR1	transcription regu	487	1.7	231	2	H83060	plasma membrane pr
415	6	1.7	194	2	S07260	histone H1 - trout	488	1.7	231	2	T12012	conserved hypothet
416	6	1.7	194	2	A45275	histone H5 - musco	489	1.7	232	2	S24390	exotoxin 12 [impor
417	6	1.7	195	1	MOHU3V	21K outer membrane	490	1.7	232	2	T03678	hypothetical prote
418	6	1.7	195	2	A42377	myosin alkali ligh	491	1.7	232	2	D87623	transforming prote
419	6	1.7	196	2	H75468	hypothetical prote	492	1.7	232	2	E89607	hypothetical prote
420	6	1.7	197	2	D70017	probable DNA polym	493	1.7	233	2	B90210	probable pkmw prot
421	6	1.7	197	2	C82601	hypothetical prote	494	1.7	233	2	A37332	alpha-1-B-glycopro
422	6	1.7	197	2	H86979	hypothetical prote	495	1.7	233	2	S05032	beta-crystallin B1
423	6	1.7	199	2	JU0052	hypothetical prote	496	1.7	237	2	F70606	hypothetical prote
424	6	1.7	199	2	C69659	puromycin N-acetyl	497	1.7	237	2	A42013	hypothetical prote
425	6	1.7	199	2	T14468	molybdopterin-guan	498	1.7	238	1	CYCHB1	thiamin-phosphate
426	6	1.7	201	2	AD0283	pollen coat protei	499	1.7	238	2	T28419	hypothetical prote
427	6	1.7	201	2	H70635	lacyl-carrier-prot	500	1.7	240	2	F98066	hypothetical prote
428	6	1.7	201	2	E95072	hypothetical prote	501	1.7	240	2	H64373	hypothetical prote
429	6	1.7	201	2	B97940	nitroreductase fam	502	1.7	241	2	S19999	hypothetical prote
430	6	1.7	201	2	SS4475	nitroreductase (EC	503	1.7	241	2	D87494	conserved hypothet
431	6	1.7	202	2	S76439	hypothetical prote	504	1.7	241	2	S53522	crystallin beta B1
432	6	1.7	202	2	F84382	hypothetical prote	505	1.7	243	2	G98156	hypothetical prote
433	6	1.7	202	2	S00747	endopeptidase Clp	506	1.7	243	2	B95885	hypothetical prote
434	6	1.7	203	2	A72705	hypothetical prote	507	1.7	244	2	T20810	hypothetical prote
435	6	1.7	204	1	STFI	somatotropin precu	508	1.7	244	2	A87505	hypothetical prote
436	6	1.7	204	2	F51289	hypothetical prote	509	1.7	244	2	T16942	flagellar L-ring p
437	6	1.7	204	2	S01746	somatotropin - Mor	510	1.7	245	1	G64834	hypothetical prote
438	6	1.7	204	2	S30491	somatotropin - Aca	511	1.7	245	2	A82195	probable fibrin
439	6	1.7	204	2	A56904	somatotropin precu	512	1.7	245	2	B84289	hypothetical prote
440	6	1.7	204	2	JC4261	somatotropin precu	513	1.7	246	1	C72109	hypothetical prote
441	6	1.7	204	2	T15274	somatotropin precu	514	1.7	246	2	D86512	IMP dehydrogenase
442	6	1.7	205	2	B87296	hypothetical prote	515	1.7	247	2	AB2465	hypothetical prote
443	6	1.7	205	2	I40812	hypothetical prote	516	1.7	247	2	S76547	hypothetical prote
444	6	1.7	206	1	HSTR1R	porphobilinogen sy	517	1.7	249	2	T35839	probable dihydrodi
445	6	1.7	206	2	C24723	histone H1 - rainb	518	1.7	250	2	C87489	biotin protein lig
446	6	1.7	208	2	S15091	trpG protein - Cor	519	1.7	250	2	D75364	hypothetical prote
447	6	1.7	208	2	H70965	homeotic protein p	520	1.7	250	2	G85015	hypothetical prote
448	6	1.7	208	2	T36390	probable phage pro	521	1.7	251	2	F83604	hypothetical prote
449	6	1.7	208	2	F71111	hypothetical prote	522	1.7	251	2	B47019	hypothetical prote
450	6	1.7	211	2	T08112	pectinesterase hom	523	1.7	253	2	G97462	hypothetical prote
451	6	1.7	211	2	AH2253	hypothetical prote	524	1.7	254	2	T36161	Cfx protein - Alc
452	6	1.7	213	2	F82211	hypothetical prote	525	1.7	254	2	T25073	hypothetical prote
453	6	1.7	215	2	T03680	probable glucathio	526	1.7	254	2	AB2681	hypothetical prote
454	6	1.7	215	2	T36448	plasma membrane pr	527	1.7	255	2	AB2109	transcription regu
455	6	1.7	215	2	B37332	probable methyltra	528	1.7	256	2	G82804	phosphatidyltransf
456	6	1.7	216	2	H69797	transforming prote	529	1.7	256	2	T21238	conserved hypothet
457	6	1.7	216	2	G10101	hypothetical prote	530	1.7	256	2	G97031	hypothetical prote
458	6	1.7	217	1	H69797	probable transcrip	531	1.7	257	2	B41843	TPR-repeat contain
459	6	1.7	219	2	T19897	hypothetical prote	532	1.7	258	2	T24035	hypothetical prote
460	6	1.7	219	2	A85855	probable transcrip	533	1.7	258	2	G96023	hypothetical prote
461	6	1.7	219	2	B64985	hypothetical 25.3	534	1.7	258	2	E87293	probable phosphona
462	6	1.7	220	2	A46597	acidic calmodulin-	535	1.7	259	2	A29831	acid phosphatase I
463	6	1.7	220	2	H90173	3-dehydroquinat d	536	1.7	259	2	A13116	heat-labile entero
464	6	1.7	221	2	B72318	hypothetical prote	537	1.7	259	2	T09415	hypothetical prote
465	6	1.7	221	2	AH0286	phage shock protei	538	1.7	261	2	AC0332	probable surface p
466	6	1.7	221	2	AB3018	thiamin-phosphate	539	1.7	261	2	AF2698	probable OmpA fam1
467	6	1.7	221	2	AB3018	thiamin-phosphate	540	1.7	262	2	AF2698	NAD/NADP dependent

541	6	1.7	263	2	T09841	hypothetical prote	614	1.7	298	2	JC7568	kidney inhibitor o
542	6	1.7	264	2	E75161	shikimate 5-dehydr	615	1.7	299	2	A99422	hypothetical prote
543	6	1.7	265	2	AH0759	propanediol diffus	616	1.7	300	2	F97277	probable glycosylt
544	6	1.7	266	2	F97086	anaerobic sulfite	617	1.7	301	2	A75599	ribokinase - Daino
545	6	1.7	267	2	T36461	hypothetical prote	618	1.7	302	2	E97380	phn7 protein (lipo
546	6	1.7	268	2	B95988	hypothetical prote	619	1.7	303	2	AD2598	conserved hypothet
547	6	1.7	269	2	D98241	hypothetical prote	620	1.7	304	2	T47557	hypothetical prote
548	6	1.7	270	2	AH3044	conserved hypothet	621	1.7	305	2	H82569	prolipo protein dia
549	6	1.7	271	2	R5H07A	ribosomal protein	622	1.7	306	2	B75509	conserved hypothet
550	6	1.7	272	2	R5H07A	ribosomal protein	623	1.7	307	2	B75509	hypothetical prote
551	6	1.7	273	2	S18159	ribosomal protein	624	1.7	308	2	A75509	probable transcript
552	6	1.7	274	2	A30241	ribosomal protein	625	1.7	309	2	AF1526	transforming prote
553	6	1.7	275	2	C90411	ketopantoate hydro	626	1.7	310	2	B95007	hypothetical prote
554	6	1.7	276	2	A87404	ribosomal protein	627	1.7	311	2	E97879	hypothetical prote
555	6	1.7	277	2	G84319	crotonine-5'-monop	628	1.7	312	2	D83479	probable transcript
556	6	1.7	278	2	F64024	hypothetical prote	629	1.7	313	2	E87479	transforming prote
557	6	1.7	279	2	T19829	hypothetical prote	630	1.7	314	2	TVH0UD	hypothetical prote
558	6	1.7	280	2	H75576	hypothetical prote	631	1.7	315	2	T16567	probable transcript
559	6	1.7	281	2	T26957	hypothetical prote	632	1.7	316	2	BVECM	hypothetical prote
560	6	1.7	282	2	C69407	hypothetical prote	633	1.7	317	2	AE0432	conserved operon per
561	6	1.7	283	2	T35961	phosphoribosylform	634	1.7	318	2	E95855	maltoase operon per
562	6	1.7	284	2	T30959	probable transcript	635	1.7	319	2	E81288	conserved hypothet
563	6	1.7	285	2	T15630	hypothetical prote	636	1.7	320	2	AD3154	hypothetical prote
564	6	1.7	286	2	T47937	hypothetical prote	637	1.7	321	2	E85112	nucleotidyltransfe
565	6	1.7	287	2	G75606	hypothetical prote	638	1.7	322	2	S25511	hypothetical 34.6
566	6	1.7	288	2	A69077	probable glycohydr	639	1.7	323	2	E91140	outer membrane pro
567	6	1.7	289	2	A70853	conserved hypothet	640	1.7	324	2	AH0906	hypothetical prote
568	6	1.7	290	2	H82488	hypothetical prote	641	1.7	325	2	B83294	hypothetical prote
569	6	1.7	291	2	B45247	NH(3)-dependent NA	642	1.7	326	2	C90277	conserved hypothet
570	6	1.7	292	2	C82273	Arac homolog ToxT	643	1.7	327	2	B87433	probable ATP-bindi
571	6	1.7	293	2	S3274	tcpN protein - Vib	644	1.7	328	2	D69881	hypothetical prote
572	6	1.7	294	2	A22295	thiosulfate sulfur	645	1.7	329	2	A61183	yabc protein homol
573	6	1.7	295	2	G71849	amino acid ABC tra	646	1.7	330	2	I40491	hypothetical prote
574	6	1.7	296	2	S71222	xyloglucan endo-1,	647	1.7	331	2	C98193	conserved hypothet
575	6	1.7	297	2	T06613	probable sugar nuc	648	1.7	332	2	AG3093	sugar transport sy
576	6	1.7	298	2	A69112	quinolinate phosph	649	1.7	333	2	B81168	hypothetical prote
577	6	1.7	299	2	E89226	hypothetical prote	650	1.7	334	2	T06053	transporter NMB070
578	6	1.7	300	2	F97034	hypothetical prote	651	1.7	335	2	C70798	probable ubiqutin
579	6	1.7	301	2	G84636	hypothetical prote	652	1.7	336	2	B99607	probable PPE prote
580	6	1.7	302	2	D84968	hypothetical prote	653	1.7	337	2	C82085	hypothetical prote
581	6	1.7	303	2	H70942	hypothetical prote	654	1.7	338	2	T31880	conserved hypothet
582	6	1.7	304	2	S78161	H+-transporting tw	655	1.7	339	2	AG0121	hypothetical prote
583	6	1.7	305	2	TU0115	genome polyprotein	656	1.7	340	2	C70136	probable sideropho
584	6	1.7	306	2	A9205	hypothetical prote	657	1.7	341	2	T49591	conserved hypothet
585	6	1.7	307	2	A82310	sulfate ABC transp	658	1.7	342	2	AE1932	probable 35 kDa r
586	6	1.7	308	2	B88349	protein Y48E1C.1	659	1.7	343	2	A99510	hypothetical prote
587	6	1.7	309	2	E88597	protein Y47D3B.6	660	1.7	344	2	A69992	hypothetical prote
588	6	1.7	310	2	T27027	hypothetical prote	661	1.7	345	2	S62810	conserved hypothet
589	6	1.7	311	2	AC2551	hypothetical prote	662	1.7	346	2	A11773	adenine specific D
590	6	1.7	312	2	D32354	fructose-bisphosph	663	1.7	347	2	E87401	butyrolactone auto
591	6	1.7	313	2	G69204	motA homolog laft	664	1.7	348	2	T08462	proline lminopepti
592	6	1.7	314	2	E40590	hypothetical prote	665	1.7	349	2	F90296	hypothetical prote
593	6	1.7	315	2	F71076	phosphate transpor	666	1.7	350	2	T35646	hypothetical prote
594	6	1.7	316	2	S72843	phosphate transpor	667	1.7	351	2	B97507	conserved hypothet
595	6	1.7	317	2	T51595	hypothetical prote	668	1.7	352	2	AF2725	probable thiamin m
596	6	1.7	318	2	JC5552	chorion protein s3	669	1.7	353	2	H86765	transcription regu
597	6	1.7	319	2	H87072	ATP-phosphoribosyl	670	1.7	354	2	S25513	L-lactate dehydrog
598	6	1.7	320	2	S30257	phosphate transpor	671	1.7	355	2	S25515	outer membrane pro
599	6	1.7	321	2	S38806	phosphate transpor	672	1.7	356	2	S25514	outer membrane pro
600	6	1.7	322	2	AE2006	phosphate transpor	673	1.7	357	2	S20032	hypothetical prote
601	6	1.7	323	2	T02543	aldehyde dehydroge	674	1.7	358	2	B95888	probable dipeptida
602	6	1.7	324	2	F82938	iron(III) dicitrat	675	1.7	359	2	A31174	iron ABC transport
603	6	1.7	325	2	T35270	hypothetical alani	676	1.7	360	2	A31607	probable transcript
604	6	1.7	326	2	F97480	probable dehydroge	677	1.7	361	2	S20494	3-oxoacyl-[acyl-ca
605	6	1.7	327	2	S09209	chorion protein s3	678	1.7	362	2	C97677	root adhesin - pse
606	6	1.7	328	2	H72378	conserved hypothet	679	1.7	363	2	A12901	probable glycerol-
607	6	1.7	329	2	D73134	probable chemotaxi	680	1.7	364	2	A49619	glycerol-3-phospha
608	6	1.7	330	2	T46617	heme O oxygenase -	681	1.7	365	2	A12901	crtA protein - Rho
609	6	1.7	331	2	D70314	conserved hypothet	682	1.7	366	2	T50744	spheroidane monoox
610	6	1.7	332	2	S55063	hypothetical prote	683	1.7	367	2	F50180	sun (fmu) protein
611	6	1.7	333	2	C82787	hypothetical prote	684	1.7	368	2	F87318	transcription regu
612	6	1.7	334	2	F81325	hypothetical prote	685	1.7	369	2	F84786	probable farnesyla
613	6	1.7	335	2	F97463	probable lysR-like	686	1.7	370	2	E83084	rod shape-determin

833	6	1.7	385	2	T22678	hypothetical prote	906	1.7	410	2	C86835	hypothetical prote
834	6	1.7	385	2	E83491	probable membrane-	907	1.7	411	2	S35333	steroid receptor p
835	6	1.7	386	2	S74778	hypothetical prote	908	1.7	411	2	A70509	hypothetical prote
836	6	1.7	386	2	B75616	conserved hypothet	909	1.7	411	2	T51818	ATP phosphoribosyl
837	6	1.7	386	2	S34672	xylose operon tran	910	1.7	412	2	D71803	ubiquinol-cytochro
838	6	1.7	388	2	S76932	alkaline serine pr	911	1.7	412	2	C64712	ubiquinol-cytochro
839	6	1.7	388	2	S76932	probable phosphori	912	1.7	413	2	B82760	cell division prot
840	6	1.7	389	1	SAVLAR	large-surface anti	913	1.7	413	2	S60930	probable membrane
841	6	1.7	389	1	SAVLBH	large-surface anti	914	1.7	413	2	A62905	sensory transducti
842	6	1.7	389	1	SAVLAI	large-surface anti	915	1.7	413	2	A82743	conserved hypothet
843	6	1.7	389	1	SAVLAI	large-surface anti	916	1.7	413	2	G69333	probable acyl-CoA
844	6	1.7	389	2	SAVLCP	large-surface anti	917	1.7	414	2	S34829	triose phosphate/3
845	6	1.7	389	2	S41871	large-surface anti	918	1.7	414	2	S23224	triose phosphate/3
846	6	1.7	389	2	S47407	surface antigen -	919	1.7	414	2	A37133	apolipoprotein A-I
847	6	1.7	389	2	S32202	surface antigen -	920	1.7	414	2	I48975	apolipoprotein A-I
848	6	1.7	389	2	S20745	large-surface anti	921	1.7	414	2	T22498	hypothetical prote
849	6	1.7	389	2	S20749	surface antigen -	922	1.7	415	2	T19099	hypothetical prote
850	6	1.7	389	2	S20749	surface antigen -	923	1.7	415	2	G64542	glycine hydroxymet
851	6	1.7	389	2	B75363	glutamate N-acetyl	924	1.7	416	2	G71965	hypothetical prote
852	6	1.7	389	2	B96635	hypothetical prote	925	1.7	416	2	G97524	hypothetical prote
853	6	1.7	389	2	I49640	transcription fact	926	1.7	417	2	G69250	hypothetical prote
854	6	1.7	389	2	G70120	outer membrane pro	927	1.7	418	2	T15142	hypothetical prote
855	6	1.7	389	2	F75411	conserved hypothet	928	1.7	419	2	T15088	hypothetical prote
856	6	1.7	390	1	DNWS53	cellular tumor ant	929	1.7	419	2	A57000	orphan receptor CO
857	6	1.7	390	1	S58814	cell division prot	930	1.7	420	2	T36272	phosphoglycerate k
858	6	1.7	390	2	T04097	acyl-[acyl-carrier	931	1.7	420	1	TVUTG4	probable glutamate
859	6	1.7	390	2	A98336	cystathionine gamm	932	1.7	420	2	A81895	envelope protein -
860	6	1.7	390	2	AT2946	methionine gamma-l	933	1.7	420	2	T42616	hypothetical prote
861	6	1.7	390	2	JS0296	transposase - Stap	934	1.7	420	2	H84890	hypothetical prote
862	6	1.7	390	2	S44285	EAR2 protein - mou	935	1.7	420	2	A71030	hypothetical prote
863	6	1.7	391	2	C84268	aspartate aminotra	936	1.7	421	1	KIUTGC	hypothetical prote
864	6	1.7	391	2	T34935	hypothetical prote	937	1.7	421	1	I64185	phosphoglycerate k
865	6	1.7	393	1	DNHU53	cellular tumor ant	938	1.7	421	1	T25205	gene II protein -
866	6	1.7	393	1	S06594	cellular tumor ant	939	1.7	421	1	T35250	citrate synthase-1
867	6	1.7	393	2	T07653	acyl-[acyl-carrier	940	1.7	421	2	A43393	bicyclomycin resis
868	6	1.7	393	2	C83155	probable MFS trans	941	1.7	421	2	H70607	hypothetical prote
869	6	1.7	394	2	T51494	stearyl-acyl carr	942	1.7	422	2	JC5524	26S proteasome reg
870	6	1.7	395	2	AD2119	hypothetical prote	943	1.7	422	2	T47901	endosperm specific
871	6	1.7	395	2	T48301	protein kinase-lik	944	1.7	422	2	I48305	gene COUP-TF1 prot
872	6	1.7	395	2	F82852	conserved hypothet	945	1.7	422	2	T06774	cell division prot
873	6	1.7	396	2	B39170	acyl-[acyl-carrier	946	1.7	423	2	S02710	transcription fact
874	6	1.7	396	2	S31959	acyl-[acyl-carrier	947	1.7	423	2	D95565	F6D8-29 [Imported]
875	6	1.7	396	2	A91019	probable antibiote	948	1.7	423	2	I40646	probable 26S prote
876	6	1.7	396	2	C85863	probable antibiote	949	1.7	424	2	T45317	sensor-like protei
877	6	1.7	397	2	S20617	transcription fact	950	1.7	424	2	H70390	hypothetical zinc-
878	6	1.7	398	1	VBBPA7	minor capsid prote	951	1.7	425	2	T38548	probable transfera
879	6	1.7	398	2	S23351	hypothetical 43.3	952	1.7	425	2	T18723	conserved hypothet
880	6	1.7	398	2	A64982	probable outer mem	953	1.7	426	2	C96676	hypothetical prote
881	6	1.7	398	2	B85851	acyl-[acyl-carrier	954	1.7	426	2	T50593	probable membrane
882	6	1.7	399	2	OHSPAD	large-surface anti	955	1.7	428	2	A05336	hypothetical prote
883	6	1.7	399	2	S24995	acyl-[acyl-carrier	956	1.7	429	2	T21060	hypothetical prote
884	6	1.7	400	1	SAVLA	large-surface anti	957	1.7	430	2	T36682	probable secreted
885	6	1.7	401	1	A36961	pilin biogenesis p	958	1.7	431	2	F83123	probable ABC tran
886	6	1.7	401	2	E84869	histidine-TRNA lig	959	1.7	431	2	B87285	phosphate ABC tran
887	6	1.7	401	2	S76788	phosphate transloc	960	1.7	432	2	E87508	probable membrane
888	6	1.7	401	2	S45583	hypothetical prote	961	1.7	432	2	D65132	histidinol dehydro
889	6	1.7	401	2	H83911	hypothetical prote	962	1.7	432	2	H90162	hypothetical prote
890	6	1.7	402	2	AD1417	drug-efflux transp	963	1.7	432	2	S20060	translation elonga
891	6	1.7	402	2	AD1417	procollagen I C-pr	964	1.7	432	2	T51237	translation elonga
892	6	1.7	402	2	AF1792	TcAB protein [impo	965	1.7	433	2	H86279	translation elonga
893	6	1.7	402	2	JH0403	diacylglycerol a	966	1.7	433	2	T46107	hypothetical prote
894	6	1.7	402	2	F90035	steroid receptor p	967	1.7	433	2	C86823	hypothetical prote
895	6	1.7	402	2	S73773	ear-2 protein - hu	968	1.7	433	2	A54595	transcription fact
896	6	1.7	403	2	S03334	hypothetical prote	969	1.7	433	2	A70587	hypothetical prote
897	6	1.7	403	2	S02709	hypothetical prote	970	1.7	433	2	T39772	preprotein translo
898	6	1.7	403	2	B70659	aminocyclase (EC 3	971	1.7	433	2	C86823	ubiquitin carboxyl
899	6	1.7	404	2	F59097	peptidase T (amino	972	1.7	433	2	C86823	sugar-binding prot
900	6	1.7	404	2	S71264	hypothetical prote	973	1.7	433	2	B72313	glutamine syntheta
901	6	1.7	407	2	A47488	acyl-[acyl-carrier	974	1.7	433	2	S20489	S-locus-specific g
902	6	1.7	408	2	E69588	hypothetical prote	975	1.7	438	1	S24085	
903	6	1.7	408	2	E69588	aminocyclase (EC 3	976	1.7	438	2	C98343	
904	6	1.7	409	2	T20847	hypothetical prote	977	1.7	439	2	B72313	
905	6	1.7	410	2	T18726	hypothetical prote	978	1.7	439	2	B72313	
						orphan receptor CO	979	1.7	439	2	B72313	

979 6 1.7 440 1 KIUTGG
 980 6 1.7 440 1 TVUTGB
 981 6 1.7 440 1 F64359
 982 6 1.7 440 2 G82436
 983 6 1.7 441 2 T35788
 984 6 1.7 442 2 S58738
 985 6 1.7 443 2 J02134
 986 6 1.7 443 2 C75617
 987 6 1.7 444 2 AC1792
 988 6 1.7 444 2 A11416
 989 6 1.7 445 2 S43492
 990 6 1.7 446 2 D71418
 991 6 1.7 447 2 T05070
 992 6 1.7 449 2 JC2381
 993 6 1.7 449 2 JC7306
 994 6 1.7 449 2 G89841
 995 6 1.7 450 2 B70318
 996 6 1.7 451 2 T02113
 997 6 1.7 452 2 D98280
 998 6 1.7 453 2 E86159
 999 6 1.7 454 1 A28955
 1000 6 1.7 456 2 F69132

ALIGNMENTS

RESULT 1
 JC6558
 outer membrane protein A precursor - Klebsiella pneumoniae
 C:Species: Klebsiella pneumoniae
 C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
 C:Accession: JC6558
 R:Nguyen, T.N.; Samuelson, P.; Sterky, F.; Merle-Poitte, C.; Robert, A.; Bausant, T.; H
 Gene 210, 93-101, 1998
 A:Title: Chromosomal sequencing using a PCR-based biotin-capture method allowed isolation
 A:Reference number: JC6558; MUID:98192544; PMID:9524233
 A:Accession: JC6558
 A:Molecule type: DNA
 A:Residues: 1-356 <NGU>
 A:Experimental source: IP 1145
 C:Genetics:
 A:Gene: ompA
 C:Superfamily: outer membrane protein A
 C:Keywords: membrane protein
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-356/Product: outer membrane protein A #status predicted <MAT>

Query Match 97.4%; Score 335; DB 2; Length 356;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 AAKPDNTWAGGKLGWSQYHDTGFGYNGFNNGPRNDQLGAGFGGYQVNPYLGFEFG 68
 DB 21 AAKPDNTWAGGKLGWSQYHDTGFGYNGFNNGPRNDQLGAGFGGYQVNPYLGFEFG 80
 QY 69 YDWLGRMAYKGVNDNGAFKAQGVQLTAKLGYPTDLDITTLRLGVMWRADSKGNVASTG 128
 DB 81 YDWLGRMAYKGVNDNGAFKAQGVQLTAKLGYPTDLDITTLRLGVMWRADSKGNVASTG 140
 QY 129 VSRSEHDTGVPFAGGVWAVTRDIATRLRYQWNNIGDAGTVTRPDNGMLSLGVSYR 188
 DB 141 VSRSEHDTGVPFAGGVWAVTRDIATRLRYQWNNIGDAGTVTRPDNGMLSLGVSYR 200
 QY 189 FGQEDAAPVVPAP 248
 DB 201 FGQEDAAPVVPAP 260
 QY 249 KGSAAVLGYTDRTIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNT 308
 DB 261 KGSAAVLGYTDRTIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNT 320
 QY 309 CDNVKARAALIDCLAPDRRVEIEVKYKEVVTOPA 343

Db 321 CDNVKARAALIDCLAPDRRVEIEVKYKEVVTOPA 355

RESULT 2

I62385
 outer membrane protein ompA - Escherichia vulneris (fragment)
 N:Alternate names: outer membrane protein II
 C:Species: Escherichia vulneris
 C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 20-Aug-1999
 C:Accession: I62385
 R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
 J. Gen. Microbiol. 137, 1911-1921, 1991
 A:Title: Molecular and evolutionary relationships among enteric bacteria.
 A:Reference number: I40701; MUID:92065252; PMID:1955870
 A:Accession: I62385
 A>Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-238 <RES>
 A:Cross-references: GB:M63348; NID:g146984; PIDN:AAA24233.1; PID:g146985
 C:Genetics:
 A:Gene: ompA
 C:Superfamily: outer membrane protein A
 C:Keywords: membrane protein
 F:98-109/Region: alanine/proline-rich

Query Match

15.4%; Score 53; DB 2; Length 238;
 Best Local Similarity 100.0%; Pred. No. 8e-46;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 213 FTLKSDVLFNFNFKATLKEGQALDQLYTOLSNMMDPKDGSAAVLGYTDRTIGSE 265
 DB 116 FTLKSDVLFNFNFKATLKEGQALDQLYTOLSNMMDPKDGSAAVLGYTDRTIGSE 168

RESULT 3

S07222
 outer membrane protein ompA precursor - Enterobacter aerogenes
 C:Species: Enterobacter aerogenes
 C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999
 C:Accession: S07222
 R:Braun, G.; Cole, S.T.
 Eur. J. Biochem. 137, 495-500, 1983
 A:Title: Molecular characterization of the gene coding for major outer membrane prote

A:Reference number: S07222; MUID:84108348; PMID:6363039
 A:Accession: S07222
 A:Molecule type: DNA
 A:Residues: 1-350 <BRA>
 A:Cross-references: EMBL:X00254; NID:g40837; PIDN:CAA25062.1; PID:g40838
 A>Note: the authors translated the codon CAG for residue 197 as Asn
 C:Genetics:
 A:Gene: ompA
 C:Superfamily: outer membrane protein A
 C:Keywords: membrane protein
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-350/Product: outer membrane protein ompA #status predicted <MAT>
 F:201-212/Region: alanine/proline-rich
 F:213-350/Domain: periplasmic #status predicted <PER>

Query Match

15.4%; Score 53; DB 2; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.1e-45;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 213 FTLKSDVLFNFNFKATLKEGQALDQLYTOLSNMMDPKDGSAAVLGYTDRTIGSE 265
 DB 219 FTLKSDVLFNFNFKATLKEGQALDQLYTOLSNMMDPKDGSAAVLGYTDRTIGSE 271

RESULT 4

I40703
 outer membrane protein A - Citrobacter freundii (fragment)
 N:Alternate names: outer membrane protein II
 C:Species: Citrobacter freundii

C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Aug-1999
 C:Accession: I40703
 R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
 J. Gen. Microbiol. 137, 1911-1921, 1991
 A:Title: Molecular and evolutionary relationships among enteric bacteria.
 A:Reference number: I40703; MUID:92065252; PMID:1955870
 A:Accession: I40703
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-238 <RES>
 A:Cross-references: GB:M63354; NID:g144441; PIDN:AA23095.1; PID:g144442
 C:Genetics:
 A:Gene: ompA
 C:Superfamily: outer membrane protein A
 C:Keywords: membrane protein
 F:99-109/Region: alanine/proline-rich

Query Match 12.5% Score 43; DB 2; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.2e-35;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 KISARGMESNPVTGTCNVKARAALDCLAPDRRVEIEVKG 334
 |||||
 DB 195 KISARGMESNPVTGTCNVKARAALDCLAPDRRVEIEVKG 337

RESULT 5
 MMECA
 outer membrane protein A precursor - Escherichia coli (strain K-12)
 C:Alternate names: outer membrane protein II*
 C:Species: Escherichia coli
 C>Date: 30-Sep-1980 #sequence_revision 30-Sep-1980 #text_change 01-Mar-2002
 C:Accession: A93707; A92862; A93855; S50909; D64836; A03434
 R:Beck, E.; Bremer, E.
 Nucleic Acids Res. 8, 3011-3024, 1980
 A:Title: Nucleotide sequence of the gene ompA coding the outer membrane protein II of Escherichia coli.
 A:Reference number: A93707; MUID:81053729; PMID:6253901
 A:Accession: A93707
 A:Molecule type: DNA
 A:Residues: 1-346 <BSC>
 A:Cross-references: GB:J01654; GB:J01654; NID:g42159; PIDN:CAA23588.1; PID:g42161
 A:Experimental source: strain K12
 R:Govva, N.R.; Nakamura, K.; Inouye, M.
 J. Mol. Biol. 143, 317-328, 1980
 A:Title: Gene structure of the OmpA protein, a major surface protein of Escherichia coli.
 A:Reference number: A92862; MUID:81170587; PMID:6260961
 A:Accession: A92862
 A:Molecule type: DNA
 A:Residues: 1-346 <MOV>
 A:Cross-references: GB:J01654; GB:V00307; GB:V00358; NID:g146979; PIDN:AAA24231.1; PID:g146979
 A:Experimental source: K12, strain K802
 R:Chen, R.; Schmidmayr, W.; Kramer, C.; Chen-Schmeisser, U.; Henning, U.
 Proc. Natl. Acad. Sci. U.S.A. 77, 4592-4596, 1980
 A:Title: Primary structure of major outer membrane protein II* (ompA protein) of Escherichia coli.
 A:Reference number: A93855; MUID:81054820; PMID:7001461
 A:Accession: A93855
 A:Molecule type: protein
 A:Residues: 22-346 <CHE>
 A:Experimental source: K12, strain P400
 R:Kuhn, A.; Klefer, D.; Koehne, C.; Zhu, H.X.; Tschantz, W.R.; Dalbey, R.E.
 Eur. J. Biochem. 226, 891-897, 1994
 A:Title: Evidence for a loop-like insertion mechanism of pro-Omp A into the inner membrane.
 A:Reference number: S50909; MUID:95112855; PMID:7813480
 A:Accession: S50909
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-46 <KH>
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: D64836

A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-346 <BLAT>
 A:Cross-references: GB:AE000198; GB:U00096; NID:g1787189; PIDN:AA274043.1; PID:g17871
 A:Experimental source: strain K-12, substrain MG1655
 C:Genetics:
 A:Gene: ompA; tolG; tut; con
 A:Map position: 22 min
 C:Function:
 A:Description: required for the action of colicins K and L and for the stabilization of diffusion channels that allow penetration of various solutes
 C:Superfamily: outer membrane protein A
 C:Keywords: membrane protein; monomer
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-346/Product: outer membrane protein A #status predicted <MAT>
 F:22-196/Domain: intramembrane #status predicted <INT>
 F:196-208/Region: alanine/proline-rich
 F:209-346/Domain: periplasmic #status predicted <PER>
 F:257-301/Domain: ompA-like domain #status predicted <OMP>

Query Match 9.6% Score 33; DB 1; Length 346;
 Best Local Similarity 100.0%; Pred. No. 2.6e-25;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 KAQGVQLTAKLGYPTDLDLDTYTRLGGMVWRAD 119
 |||||
 DB 94 KAQGVQLTAKLGYPTDLDLDTYTRLGGMVWRAD 126

RESULT 6
 A90759
 outer membrane protein 3a ECs1041 [imported] - Escherichia coli (strain O157:H7, substrain ECs1041)
 C:Species: Escherichia coli
 C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 01-Mar-2002
 C:Accession: A90759
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.; Sasagawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and 9 other strains.
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: A90759
 A:Molecule type: DNA
 A:Residues: 1-346 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BA034464.1; PID:g13360501; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RMD 050952
 C:Genetics:
 A:Gene: ECs1041
 C:Superfamily: outer membrane protein A

Query Match 9.6% Score 33; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 2.6e-25;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 KAQGVQLTAKLGYPTDLDLDTYTRLGGMVWRAD 119
 |||||
 DB 94 KAQGVQLTAKLGYPTDLDLDTYTRLGGMVWRAD 126

RESULT 7
 G85622
 outer membrane protein 3a [imported] - Escherichia coli (strain O157:H7, substrain ECs1041)
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 01-Mar-2002
 C:Accession: G85622
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May, A.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda, Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: G85622
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-346 <STO>
A:Cross-references: GB:AE005174; NID:gl2514142; PIDN:AAG55443.1; GSPDB:GN00145; UWGP:213
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A

Query Match 9.6%; Score 33; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.6e-25;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 KAQGVQLTAKLGYPTDLDIYTRLGGMVVRAD 119
|||||
Db 94 KAQGVQLTAKLGYPTDLDIYTRLGGMVVRAD 126

RESULT 8
I62386
outer membrane protein A - Escherichia hermannii (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia hermannii
C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 04-Mar-2000
A:Accession: I62386; I62390
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: 140701; MUID:92065252; PMID:1955870
A:Accession: I62386
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-243 <RES>
A:Cross-references: GB:M63346; NID:gl146986; PIDN:AAA24234.1; PID:gl146987
A:Accession: I62390
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-243 <RES>
A:Cross-references: GB:M63347; NID:gl146994; PIDN:AAA24238.1; PID:gl146995
A:Experimental source: ATCC 33652
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:103-114/Region: alanine/proline-rich

Query Match 8.4%; Score 29; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 TKHFTLSKDVLFNFNFKATLKPEGQQALDQ 238
|||||
Db 118 TKHFTLSKDVLFNFNFKATLKPEGQQALDQ 146

RESULT 9
I62389
outer membrane protein ompA - Escherichia vulneris (ATCC 33821) (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia vulneris
A:Variety: ATCC 33821
C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 20-Aug-1999
C:Accession: I62389
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: 140701; MUID:92065252; PMID:1955870
A:Accession: I62389
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-244 <RES>
A:Cross-references: GB:M63349; NID:gl146992; PIDN:AAA24237.1; PID:gl146993
A:Experimental source: ATCC 33821
C:Genetics:
A:Gene: ompA

C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:104-115/Region: alanine/proline-rich

Query Match 8.4%; Score 29; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 2.3e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 TKHFTLSKDVLFNFNFKATLKPEGQQALDQ 238
|||||
Db 119 TKHFTLSKDVLFNFNFKATLKPEGQQALDQ 147

RESULT 10
I62393
outer membrane protein ompA - Escherichia vulneris (ATCC 33822) (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia vulneris
A:Variety: ATCC 33822
C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 20-Aug-1999
C:Accession: I62393
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: 140701; MUID:92065252; PMID:1955870
A:Accession: I62393
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-244 <RES>
A:Cross-references: GB:M63350; NID:gl147000; PIDN:AAA24241.1; PID:gl147001
A:Experimental source: ATCC 33822
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:104-115/Region: alanine/proline-rich

Query Match 8.4%; Score 29; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 2.3e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 TKHFTLSKDVLFNFNFKATLKPEGQQALDQ 238
|||||
Db 119 TKHFTLSKDVLFNFNFKATLKPEGQQALDQ 147

RESULT 11
I84531
outer membrane protein A - Escherichia fergusonii (ATCC 35469) (fragment)
N:Alternate names: outer membrane protein II
C:Species: Escherichia fergusonii
A:Variety: ATCC 35469
C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 20-Aug-1999
C:Accession: I84531
R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A:Title: Molecular and evolutionary relationships among enteric bacteria.
A:Reference number: 140701; MUID:92065252; PMID:1955870
A:Accession: I84531
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-243 <RES>
A:Cross-references: GB:M63351; NID:gl146982; PIDN:AAA24232.1; PID:gl146983
A:Experimental source: ATCC 35469
C:Genetics:
A:Gene: ompA
C:Superfamily: outer membrane protein A
C:Keywords: membrane protein
F:103-114/Region: alanine/proline-rich

Query Match 7.8%; Score 27; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 LTKALGYPIITDDLDIYTRLGGMWRAD 119
 |||||
 Db 1 LTKALGYPIITDDLDIYTRLGGMWRAD 27

RESULT 12

MMEBAT

outer membrane protein A - Escherichia fergusonii (ATCC 35472) (fragment)
 N:Alternate names: outer membrane protein II
 C:Species: Escherichia fergusonii
 A:Variety: ATCC 35472
 C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 04-Mar-2000
 C:Accession: I62388; I62392
 R:Lawrence, J.G.; Ochman, H.; Hartl, D.L.
 J. Gen. Microbiol. 137, 1911-1921, 1991
 A:Title: Molecular and evolutionary relationships among enteric bacteria.
 A:Reference number: I40701; MUID:92065252; PMID:1955870
 A:Accession: I62388
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-243 <RES>
 A:Cross-references: GB:M63352; NID:gl46990; PIDN:AAA24236.1; PID:gl46991
 A:Experimental source: ATCC 35471
 A:Accession: I62392
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-243 <RE2>
 A:Cross-references: GB:M63353; NID:gl46998; PIDN:AAA24240.1; PID:gl46999
 A:Experimental source: ATCC 35472
 C:Genetics:
 A:Gene: ompA
 C:Superfamily: outer membrane protein A
 C:Keywords: membrane protein
 F:103-114/Region: alanine/proline-rich

Query Match 7.8%; Score 27; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 2.5e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 LTKALGYPIITDDLDIYTRLGGMWRAD 119
 |||||
 Db 1 LTKALGYPIITDDLDIYTRLGGMWRAD 27

RESULT 13

MMEBAT

outer membrane protein A precursor - Shigella dysenteriae
 C:Species: Shigella dysenteriae
 C:Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
 C:Accession: A03435
 R:Braun, G.; Cole, S.T.
 Nucleic Acids Res. 10, 2367-2378, 1982
 A:Title: The nucleotide sequence coding for major outer membrane protein OmpA of Shigella
 A:Reference number: A03435; MUID:82221414; PMID:6283478
 A:Accession: A03435
 A:Molecule type: DNA
 A:Residues: 1-351 <BRA>
 A:Cross-references: GB:V01344; NID:g46943; PIDN:CAA24638.1; PID:g46945
 C:Genetics:
 A:Gene: ompA
 C:Superfamily: outer membrane protein A
 C:Keywords: transmembrane protein
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-351/Product: outer membrane protein A #status predicted <MAT>
 F:22-201/Domain: intramembrane #status predicted <INT>
 F:201-213/Region: alanine/proline-rich
 F:214-351/Domain: periplasmic #status predicted <PER>

Query Match 7.0%; Score 24; DB 1; Length 351;
 Best Local Similarity 100.0%; Pred. No. 3.0e-16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 TKHFTLKSVDLNFENKATLKPEQG 233
 |||||
 Db 217 TKHFTLKSVDLNFENKATLKPEQG 240

RESULT 14

MMEBAT

outer membrane protein A precursor - Salmonella typhimurium
 N:Alternate names: outer membrane major heat-modifiable protein; outer membrane prote
 C:Species: Salmonella typhimurium
 C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 16-Jul-1999
 C:Accession: A03436
 R:Freudl, R.; Cole, S.T.
 Eur. J. Biochem. 134, 497-502, 1983
 A:Title: Cloning and molecular characterization of the ompA gene from Salmonella typh
 A:Reference number: A03436; MUID:83287368; PMID:6349993
 A:Accession: A03436
 A:Molecule type: DNA
 A:Residues: 1-350 <PRE>
 A:Cross-references: GB:X02006; NID:g47798; PIDN:CAA26037.1; PID:g758341
 C:Genetics:
 A:Gene: ompA
 A:Map position: 20 min
 C:Function:
 A:Description: required for the action of colicins and for the stabilization of mat
 A:Note: cannot serve as the receptor for the ompA-specific phages K3 and TuII
 C:Superfamily: outer membrane protein A
 C:Keywords: transmembrane protein
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-350/Product: outer membrane protein A #status predicted <MAT>
 F:22-200/Domain: intramembrane #status predicted <INT>
 F:200-212/Region: alanine/proline-rich
 F:213-350/Domain: periplasmic #status predicted <PER>

Query Match 6.4%; Score 22; DB 1; Length 350;
 Best Local Similarity 100.0%; Pred. No. 4.2e-14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 KISARGMGESNPVTGNTCDNVK 313
 |||||
 Db 298 KISARGMGESNPVTGNTCDNVK 319

outer membrane protein A STY1091 [Imported] - Salmonella enterica subsp. enterica ser
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 01-Mar-2002
 C:Accession: A10626
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
 th, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
 A:Reference number: AB0502; PMID:11677608
 A:Accession: A10626
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-350 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD08196.1; PID:gl6502245; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY1091
 C:Superfamily: outer membrane protein A

Query Match 6.4%; Score 22; DB 1; Length 350;
 Best Local Similarity 100.0%; Pred. No. 4.2e-14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 KISARGMGESNPVTGNTCDNVK 313
 |||||
 Db 298 KISARGMGESNPVTGNTCDNVK 319

RESULT 15

A10626

outer membrane protein A STY1091 [Imported] - Salmonella enterica subsp. enterica ser
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 01-Mar-2002
 C:Accession: A10626
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
 th, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
 A:Reference number: AB0502; PMID:11677608
 A:Accession: A10626
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-350 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD08196.1; PID:gl6502245; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY1091
 C:Superfamily: outer membrane protein A

Query Match 6.4%; Score 22; DB 2; Length 350;
 Best Local Similarity 100.0%; Pred. No. 4.2e-14;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 KISARGMGESNPVTGNTCDNVK 313
 |||||
 Db 298 KISARGMGESNPVTGNTCDNVK 319

Tue Apr 15 09:25:25 2003

us-09-831-061-2.oligo.rpr

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Search completed: April 15, 2003, 08:56:51
Job time : 53 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 15, 2003, 08:49:29 ; Search time 14 Seconds
(without alignments)
1019.133 Million cell updates/sec

Title: US-09-831-061-2
Perfect score: 344
Sequence: 1 MKAIFVLNAPKDNTHYAGG.....DRRVEIEVKYKEVVTQAG 344

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 5

Total number of hits satisfying chosen parameters: 8372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	342	99.4	344	1	OMPA_KLEPN
2	53	15.4	350	1	OMPA_ENTAE
3	43	12.5	238	1	OMPA_CITFR
4	33	9.6	346	1	OMPA_ECOLI
5	29	8.4	243	1	OMPA_ESCHE
6	27	7.8	243	1	OMPA_ESCHE
7	24	7.0	351	1	OMPA_SHIDY
8	22	6.4	350	1	OMPA_SALTY
9	20	5.8	241	1	OMPA_ESCBL
10	19	5.5	359	1	OMPA_SERMA
11	17	4.9	243	1	OMPA_SPROD
12	12	3.5	349	1	OMPA_BUCAT
13	10	2.9	353	1	OM52_HAEIN
14	10	2.9	359	1	OM53_HAEIN
15	9	2.6	186	1	MLEI_MUGCA
16	9	2.6	192	1	MLEF_RAT
17	9	2.6	196	1	MLEF_HUMAN
18	9	2.6	383	1	NRL1_RHOB
19	9	2.6	458	1	ARLY_VIBCH
20	9	2.6	1061	1	RNE_ECOLI
21	9	2.6	1576	1	YLK3_CAEEL
22	9	2.6	3866	1	HRX_MOUSE
23	8	2.3	28	1	OMPA_YERPS
24	8	2.3	51	1	LB2_TETH
25	8	2.3	94	1	YBZH_ECOLI
26	8	2.3	187	1	MLEI_MOUSE
27	8	2.3	188	1	MLEI_RAT
28	8	2.3	190	1	MLEI_CHICK
29	8	2.3	191	1	MLEI_HABIT
30	8	2.3	193	1	MLEI_RABIT
31	8	2.3	252	1	CRBL_BOVIN
32	8	2.3	260	1	HIL_VOLCA
33	8	2.3	313	1	EBAG_STRPL

34	8	2.3	316	1	CDNC_HUMAN
35	8	2.3	344	1	YHJA_YEAST
36	8	2.3	346	1	RA_HUMAN
37	8	2.3	353	1	OM51_HAEIN
38	8	2.3	355	1	FKB8_HUMAN
39	8	2.3	355	1	FKB8_MOUSE
40	8	2.3	423	1	CCG8_MOUSE
41	8	2.3	426	1	ASDA_NEUCR
42	8	2.3	437	1	BF1H_XENLA
43	8	2.3	439	1	XP2_XENLA
44	8	2.3	498	1	DGT1_MOUSE
45	8	2.3	498	1	DGT1_RAT
46	8	2.3	524	1	P60_LISWE
47	8	2.3	547	1	SPAK_HUMAN
48	8	2.3	551	1	TF65_HUMAN
49	8	2.3	553	1	ODP2_ALCEU
50	8	2.3	553	1	SPAK_RAT
51	8	2.3	556	1	SPAK_MOUSE
52	8	2.3	595	1	DCOA_KLEPN
53	8	2.3	603	1	NMBL_MOUSE
54	8	2.3	609	1	NMBL_HUMAN
55	8	2.3	622	1	3BP1_HUMAN
56	8	2.3	642	1	MB11_ARATH
57	8	2.3	676	1	ICPO_HSVBJ
58	8	2.3	676	1	ICPO_HSVBK
59	8	2.3	803	1	2XDB_HUMAN
60	8	2.3	806	1	MK07_MOUSE
61	8	2.3	1051	1	TE1A_MOUSE
62	8	2.3	1300	1	SAL3_HUMAN
63	8	2.3	1385	1	CTAL_MOUSE
64	8	2.3	2774	1	MAPA_RAT
65	7	2.0	14	1	LPW_ECOLI
66	7	2.0	66	1	Y7KD_STRLI
67	7	2.0	96	1	SY20_HUMAN
68	7	2.0	105	1	Y756_RICPR
69	7	2.0	133	1	NL21_PARJU
70	7	2.0	138	1	BCCP_HAEIN
71	7	2.0	155	1	NC33_PARJU
72	7	2.0	157	1	HES2_MOUSE
73	7	2.0	173	1	HES2_HUMAN
74	7	2.0	208	1	SPC3_STRPU
75	7	2.0	212	1	IF3_DSTRU
76	7	2.0	238	1	MNBA_WAIZE
77	7	2.0	243	1	RS3_SYN6
78	7	2.0	247	1	FMT_VIBAL
79	7	2.0	256	1	Y107_NPVOP
80	7	2.0	288	1	KLFD_HUMAN
81	7	2.0	289	1	KLFD_MOUSE
82	7	2.0	289	1	YFK2_YEAST
83	7	2.0	310	1	PR28_MYCTU
84	7	2.0	317	1	RSP4_URECA
85	7	2.0	325	1	MODD_MYCBO
86	7	2.0	325	1	MODD_MYCTU
87	7	2.0	329	1	TAL_MOUSE
88	7	2.0	331	1	TAL_HUMAN
89	7	2.0	337	1	NCA3_YEAST
90	7	2.0	345	1	CEBB_HUMAN
91	7	2.0	349	1	SCA3_MOUSE
92	7	2.0	351	1	VP39_NPVOP
93	7	2.0	354	1	PROW_SALTY
94	7	2.0	362	1	KLFI_HUMAN
95	7	2.0	370	1	KIT_FSVH2
96	7	2.0	379	1	AMPI_SCHPO
97	7	2.0	416	1	MTPI_PSYTA
98	7	2.0	457	1	ARLY_ECO57
99	7	2.0	457	1	ARLY_ECOLI
100	7	2.0	457	1	ARLY_PASNU
101	7	2.0	457	1	ARLY_FERPE
102	7	2.0	457	1	V51K_ACLSA
103	7	2.0	458	1	ARLY_SALTI
104	7	2.0	458	1	ARLY_SALTY
105	7	2.0	473	1	BIAR_CANFA
106	7	2.0	474	1	CBF5_SCHPO

P49918	homo sapien
P38768	saccharomyc
O92v3	homo sapien
P43840	haemophilus
Q14318	homo sapien
O35465	mus musculus
O8vhw2	mus musculus
O9hev5	neurospora
P13735	xenopus lae
P17437	xenopus lae
O922a7	mus musculus
O92m3	rattus norv
Q01839	listeria we
Q9uew8	homo sapien
O4206	homo sapien
O59098	alcaligenes
O88506	rattus norv
O921w9	mus musculus
P13187	klebsiella
O08919	mus musculus
O9y0r0	homo sapien
O9y313	homo sapien
O9sav1	arabidopsis
P29128	bovine herp
P29836	bovine herp
P8169	homo sapien
O9vva8	mus musculus
O64127	mus musculus
O9bxa9	homo sapien
O54991	mus musculus
P34926	rattus norv
P3053	escherichia
P22401	streptomyce
P78556	homo sapien
O92c14	rickettsia
P55958	parietaria
O40905	parietaria
P43874	haemophilus
O54792	mus musculus
O9v543	homo sapien
P16537	strongyloce
O9rsn7	deinococcus
P38564	zebra mays (m
O24695	synecococc
O87726	vibrio algi
O10346	orgyia psau
O942v9	h. krueppel-
O91jz6	mus musculus
P43607	saccharomyc
P71697	mycobacteri
P38981	urechis cau
O30620	mycobacteri
O50906	mycobacteri
P22091	mus musculus
P17542	homo sapien
P46555	saccharomyc
P17676	homo sapien
O35609	mus musculus
P17500	orgyia psau
P17327	salmonella
Q13351	homo sapien
P04048	feline sarc
O59730	schizosacch
O33481	psychrobact
O8x730	escherichia
P11447	escherichia
P57909	pasteurella
Q8za88	yersinia pe
P54892	apple chlor
Q8z311	salmonella
O8zkl6	salmonella
P79148	canis famil
O14007	schizosacch

107	7	2.0	493	1	RP54_ALCEU	P28615	alcaligenes	180	1.7	169	1	HBL2_ORYSA	O04985	oryza sativ
108	7	2.0	497	1	FXD2_HUMAN	O60548	homo sapien	181	1.7	172	1	NU6M_URILO	P3208	uria lomvia
109	7	2.0	515	1	ROCA_BACSU	P39634	bacillus su	182	1.7	173	1	NU6M_AETCR	P3189	aethia cris
110	7	2.0	516	1	P60_ENTFC	P31692	enterococcu	183	1.7	173	1	NU6M_AETPU	P43190	aethia pui
111	7	2.0	523	1	P60_LISSE	Q01838	listeria se	184	1.7	173	1	NU6M_AETPY	P43191	aethia pygm
112	7	2.0	524	1	P60_LISIV	Q01837	listeria iv	185	1.7	173	1	NU6M_ALLAL	P43192	alle alle (
113	7	2.0	527	1	HSF8_LYCP	P41153	lycopersico	186	1.7	173	1	NU6M_CALMA	P43196	calloris ma
114	7	2.0	551	1	CBX4_MOUSE	O55187	mus musculus	187	1.7	173	1	NU6M_CEPKO	P43197	cepphus gry
115	7	2.0	582	1	SPH2_HUMAN	Q92777	homo sapien	188	1.7	173	1	NU6M_CXCP	P43198	cepphus col
116	7	2.0	617	1	SYN2_MOUSE	Q92777	homo sapien	189	1.7	173	1	NU6M_CXCP	P43199	cycloclorhinc
117	7	2.0	633	1	PN22_HUMAN	Q961d6	homo sapien	190	1.7	173	1	NU6M_FRAAR	P43200	fratercula
118	7	2.0	649	1	FAF1_RAT	Q924K2	rattus norv	191	1.7	173	1	NU6M_FRAAR	P43201	fratercula
119	7	2.0	721	1	EZBE_HUMAN	Q13144	homo sapien	192	1.7	173	1	NU6M_FRAAR	P43202	fratercula
120	7	2.0	766	1	AFSL1_YEAS	P20134	saccharomyc	193	1.7	173	1	NU6M_LUNCI	P43203	lunda cirrh
121	7	2.0	799	1	AFSL1_YEAS	P54741	streptomyce	194	1.7	173	1	NU6M_LUNCI	P43204	pythoromph
122	7	2.0	799	1	AFSL1_YEAS	P54741	streptomyce	195	1.7	173	1	NU6M_LUNCI	P43205	pythoromph
123	7	2.0	809	1	PAT3_CAEEL	Q27874	caenorhabdi	196	1.7	173	1	NU6M_STRCA	Q21407	struthio ca
124	7	2.0	815	1	MK07_HUMAN	Q13164	homo sapien	197	1.7	173	1	NU6M_SYNNY	P43206	synthlibora
125	7	2.0	830	1	GCL2_MOUSE	Q92777	homo sapien	198	1.7	173	1	NU6M_SYNNY	P55734	escherichia
126	7	2.0	837	1	GCL2_MOUSE	Q92777	homo sapien	199	1.7	173	1	NU6M_SYNNY	P55734	escherichia
127	7	2.0	882	1	GND5_MOUSE	Q92830	homo sapien	200	1.7	173	1	NU6M_SYNNY	P13589	r pituitary
128	7	2.0	882	1	IF2_CHLTR	Q03385	mus musculus	201	1.7	173	1	NU6M_SYNNY	O05261	mycobacteri
129	7	2.0	914	1	GND5_HUMAN	O84098	chlamydia t	202	1.7	173	1	NU6M_SYNNY	P02258	anser anser
130	7	2.0	950	1	DC12_DROME	Q12967	homo sapien	203	1.7	173	1	NU6M_SYNNY	P06513	cairina mos
131	7	2.0	960	1	KIT_CHICK	P18170	drosophila	204	1.7	173	1	NU6M_SYNNY	P02254	salmo trutt
132	7	2.0	972	1	KFMS_HUMAN	Q08156	gallus gall	205	1.7	173	1	NU6M_SYNNY	P08590	homo sapien
133	7	2.0	975	1	KIT_CANFA	P07333	homo sapien	206	1.7	173	1	NU6M_SYNNY	Q05146	bordelella
134	7	2.0	975	1	KIT_MOUSE	O97799	canis famil	207	1.7	173	1	NU6M_SYNNY	Q31701	bacillus su
135	7	2.0	975	1	KIT_MOUSE	P05532	mus musculus	208	1.7	173	1	NU6M_SYNNY	P13249	streptomyce
136	7	2.0	977	1	KFMS_MOUSE	P10721	homo sapien	209	1.7	173	1	NU6M_SYNNY	Q8260	versinia pe
137	7	2.0	977	1	KFMS_MOUSE	P05581	mus musculus	210	1.7	173	1	NU6M_SYNNY	P38429	saccharomyc
138	7	2.0	978	1	KFMS_MOUSE	P43481	bos taurus	211	1.7	173	1	NU6M_SYNNY	P74467	synecocyst
139	7	2.0	978	1	KFMS_MOUSE	Q00495	rattus norv	212	1.7	173	1	NU6M_SYNNY	P08591	pagrus majo
140	7	2.0	980	1	KIT_CAPHI	Q28317	capra hircu	213	1.7	173	1	NU6M_SYNNY	Q01282	acanthopagr
141	7	2.0	980	1	KIT_FELCA	P13369	felis silve	214	1.7	173	1	NU6M_SYNNY	P45654	acanthopagr
142	7	2.0	1016	1	KFMS_FELCA	P13369	felis silve	215	1.7	173	1	NU6M_SYNNY	Q01283	lates calca
143	7	2.0	1083	1	T2D3_HUMAN	O84880	chlamydia t	216	1.7	173	1	NU6M_SYNNY	P48248	morone saxa
144	7	2.0	1095	1	PIPA_DROME	O00268	homo sapien	217	1.7	173	1	NU6M_SYNNY	Q89ev3	perca flave
145	7	2.0	1123	1	DC11_DROME	P13217	drosophila	218	1.7	173	1	NU6M_SYNNY	Q91b11	sciaenops o
146	7	2.0	1125	1	MD1_BORBU	O51568	borrelia bu	219	1.7	173	1	NU6M_SYNNY	P09539	seriola qui
147	7	2.0	1131	1	YAB9_YEAS	P31380	saccharomyc	220	1.7	173	1	NU6M_SYNNY	P09539	seriola qui
148	7	2.0	1147	1	YAB9_YEAS	P19706	acanthamoeb	221	1.7	173	1	NU6M_SYNNY	Q98uf6	trichogaste
149	7	2.0	1239	1	V120_EBV	P03189	epstein-bar	222	1.7	173	1	NU6M_SYNNY	P52975	caulobacter
150	7	2.0	1274	1	MYPC_HUMAN	O14896	homo sapien	223	1.7	173	1	NU6M_SYNNY	P06350	oncorhynch
151	7	2.0	1298	1	VGR3_HUMAN	P35916	homo sapien	224	1.7	173	1	NU6M_SYNNY	P34766	caenorhabdi
152	7	2.0	1323	1	LT23_CAEEL	P24348	caenorhabdi	225	1.7	173	1	NU6M_SYNNY	P06558	corynebacte
153	7	2.0	1487	1	ICP4_HSVB	P28925	equine herp	226	1.7	173	1	NU6M_SYNNY	P08685	tenebrio mo
154	7	2.0	1487	1	ICP4_HSVB	P17473	equine herp	227	1.7	173	1	NU6M_SYNNY	P34357	caenorhabdi
155	7	2.0	1589	1	DC13_DROME	P18171	drosophila	228	1.7	173	1	NU6M_SYNNY	Q05175	rattus norv
156	7	2.0	1618	1	NEST_HUMAN	P48681	homo sapien	229	1.7	173	1	NU6M_SYNNY	P33023	escherichia
157	7	2.0	2156	1	RRPL_PUUMH	P27176	pumala vir	230	1.7	173	1	NU6M_SYNNY	Q98014	sulfolobus
158	7	2.0	2220	1	CABI_HUMAN	Q96610	homo sapien	231	1.7	173	1	NU6M_SYNNY	P23853	escherichia
159	6	1.7	38	1	H5_COLLI	P02260	columba liv	232	1.7	173	1	NU6M_SYNNY	Q64757	avian adeno
160	6	1.7	72	1	SAS1_SPOHA	Q00213	sporosarcin	233	1.7	173	1	NU6M_SYNNY	P23853	escherichia
161	6	1.7	78	1	ACP_MYAXA	Q06059	anas platyr	234	1.7	173	1	NU6M_SYNNY	Q9h442	thermoplasm
162	6	1.7	81	1	NU6M_ANAPL	P80921	myxococcus	235	1.7	173	1	NU6M_SYNNY	P24069	pseudomonas
163	6	1.7	88	1	CU70_LOCOM	P80232	locusta mig	236	1.7	173	1	NU6M_SYNNY	P40265	glyptotendi
164	6	1.7	92	1	VP10_NPVOP	P08357	orgyia pseu	237	1.7	173	1	NU6M_SYNNY	P49788	homo sapien
165	6	1.7	113	1	RS6_SVNY3	P73636	synecocyst	238	1.7	173	1	NU6M_SYNNY	Q10014	caenorhabdi
166	6	1.7	115	1	VY1_TYICA	P36282	tomato yell	239	1.7	173	1	NU6M_SYNNY	Q00709	gallus gall
167	6	1.7	118	1	RL7_MCLU	P02395	micrococcus	240	1.7	173	1	NU6M_SYNNY	Q9ux20	sulfolobus
168	6	1.7	121	1	KDGL_ECOLI	P00556	escherichia	241	1.7	173	1	NU6M_SYNNY	Q10014	caenorhabdi
169	6	1.7	122	1	IN17_HUMAN	P40305	homo sapien	242	1.7	173	1	NU6M_SYNNY	Q02664	glyptotendi
170	6	1.7	126	1	CU24_ARADI	P80516	araneus dia	243	1.7	173	1	NU6M_SYNNY	Q9ux20	sulfolobus
171	6	1.7	129	1	RL7_CHLMU	P80001	chlamydia m	244	1.7	173	1	NU6M_SYNNY	Q00709	gallus gall
172	6	1.7	129	1	RL7_CHLTR	Q84318	chlamydia t	245	1.7	173	1	NU6M_SYNNY	Q9ux20	sulfolobus
173	6	1.7	139	1	YL92_MYCTU	Q10406	mycobacteri	246	1.7	173	1	NU6M_SYNNY	Q9ux20	sulfolobus
174	6	1.7	142	1	YL22_ARCFU	Q28158	archaeoglob	247	1.7	173	1	NU6M_SYNNY	Q9ux20	sulfolobus
175	6	1.7	143	1	RS12_HORVU	Q9xhs0	hordeum vul	248	1.7	173	1	NU6M_SYNNY	Q9ux20	sulfolobus
176	6	1.7	153	1	YC15_CAUCR	Q9a8v2	caulobacter	249	1.7	173	1	NU6M_SYNNY	Q9ux20	sulfolobus
177	6	1.7	154	1	YGG9_YEAS	P53162	saccharomyc	250	1.7	173	1	NU6M_SYNNY	Q9ux20	sulfolobus
178	6	1.7	157	1	CU19_LOCOM	P45593	locusta mig	251	1.7	173	1	NU6M_SYNNY	Q9ux20	sulfolobus
179	6	1.7	159	1	CU57_ARADI	P80519	araneus dia	252	1.7	173	1	NU6M_SYNNY	Q9ux20	sulfolobus

253	1	1.7	250	1	1.7	326	6	1.7	353	1	PSBA_CUSRE	P32036	cuscata_ref
254	1	1.7	254	1	1.7	327	6	1.7	353	1	PSBA_MAGPY	O98735	magnolia py
255	1	1.7	255	1	1.7	328	6	1.7	353	1	PSBA_MEDSA	P04998	medicago sa
256	1	1.7	256	1	1.7	329	6	1.7	353	1	PSBA_ORYSA	P12094	oryza sativ
257	1	1.7	257	1	1.7	330	6	1.7	353	1	PSBA_TORAC	P04848	nicotiana t
258	1	1.7	258	1	1.7	331	6	1.7	353	1	PSBA_VICFA	P13910	vicia faba
259	1	1.7	259	1	1.7	332	6	1.7	353	1	PSBA_VIGUN	Q3282	vigna ungu
260	1	1.7	260	1	1.7	333	6	1.7	353	1	PSBA_VIGUN	P51106	ordeum vul
261	1	1.7	261	1	1.7	334	6	1.7	354	1	PSBA_VIGUN	P05053	trypanosoma
262	1	1.7	262	1	1.7	335	6	1.7	354	1	PSBA_VIGUN	Q26736	trypanosoma
263	1	1.7	263	1	1.7	336	6	1.7	355	1	PSBA_VIGUN	P45370	c poly-beta
264	1	1.7	264	1	1.7	337	6	1.7	355	1	PSBA_VIGUN	P45366	t poly-beta
265	1	1.7	265	1	1.7	338	6	1.7	355	1	PSBA_VIGUN	P30692	neisseria s
266	1	1.7	266	1	1.7	339	6	1.7	355	1	PSBA_VIGUN	P55278	bacillus su
267	1	1.7	267	1	1.7	340	6	1.7	355	1	PSBA_VIGUN	Q9h778	pseudomonas
268	1	1.7	268	1	1.7	341	6	1.7	355	1	PSBA_VIGUN	P57127	buchnera ap
269	1	1.7	269	1	1.7	342	6	1.7	355	1	PSBA_VIGUN	Q29715	archaeoglob
270	1	1.7	270	1	1.7	343	6	1.7	355	1	PSBA_VIGUN	Q24648	drosophila
271	1	1.7	271	1	1.7	344	6	1.7	355	1	PSBA_VIGUN	P34735	pichia angu
272	1	1.7	272	1	1.7	345	6	1.7	355	1	PSBA_VIGUN	P49669	trypanosoma
273	1	1.7	273	1	1.7	346	6	1.7	355	1	PSBA_VIGUN	P42712	streptomyce
274	1	1.7	274	1	1.7	347	6	1.7	355	1	PSBA_VIGUN	P13772	oryctolagus
275	1	1.7	275	1	1.7	348	6	1.7	355	1	PSBA_VIGUN	Q12708	sclerotinia
276	1	1.7	276	1	1.7	349	6	1.7	355	1	PSBA_VIGUN	Q48019	mycobacteri
277	1	1.7	277	1	1.7	350	6	1.7	355	1	PSBA_VIGUN	P06138	escherichia
278	1	1.7	278	1	1.7	351	6	1.7	355	1	PSBA_VIGUN	P57308	buchnera ap
279	1	1.7	279	1	1.7	352	6	1.7	355	1	PSBA_VIGUN	O51929	buchnera ap
280	1	1.7	280	1	1.7	353	6	1.7	355	1	PSBA_VIGUN	Q9a1a4	sodalis glo
281	1	1.7	281	1	1.7	354	6	1.7	355	1	PSBA_VIGUN	P74724	synchocyst
282	1	1.7	282	1	1.7	355	6	1.7	355	1	PSBA_VIGUN	P58953	drosophila
283	1	1.7	283	1	1.7	356	6	1.7	355	1	PSBA_VIGUN	P24025	hepatitis b
284	1	1.7	284	1	1.7	357	6	1.7	355	1	PSBA_VIGUN	P12911	hepatitis b
285	1	1.7	285	1	1.7	358	6	1.7	355	1	PSBA_VIGUN	P03138	hepatitis b
286	1	1.7	286	1	1.7	359	6	1.7	355	1	PSBA_VIGUN	Q9r10	deinococcus
287	1	1.7	287	1	1.7	360	6	1.7	355	1	PSBA_VIGUN	P43136	mus musculus
288	1	1.7	288	1	1.7	361	6	1.7	355	1	PSBA_VIGUN	O09017	rattus norv
289	1	1.7	289	1	1.7	362	6	1.7	355	1	PSBA_VIGUN	P45498	staphylococ
290	1	1.7	290	1	1.7	363	6	1.7	355	1	PSBA_VIGUN	P03340	mus musculus
291	1	1.7	291	1	1.7	364	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
292	1	1.7	292	1	1.7	365	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
293	1	1.7	293	1	1.7	366	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
294	1	1.7	294	1	1.7	367	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
295	1	1.7	295	1	1.7	368	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
296	1	1.7	296	1	1.7	369	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
297	1	1.7	297	1	1.7	370	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
298	1	1.7	298	1	1.7	371	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
299	1	1.7	299	1	1.7	372	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
300	1	1.7	300	1	1.7	373	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
301	1	1.7	301	1	1.7	374	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
302	1	1.7	302	1	1.7	375	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
303	1	1.7	303	1	1.7	376	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
304	1	1.7	304	1	1.7	377	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
305	1	1.7	305	1	1.7	378	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
306	1	1.7	306	1	1.7	379	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
307	1	1.7	307	1	1.7	380	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
308	1	1.7	308	1	1.7	381	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
309	1	1.7	309	1	1.7	382	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
310	1	1.7	310	1	1.7	383	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
311	1	1.7	311	1	1.7	384	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
312	1	1.7	312	1	1.7	385	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
313	1	1.7	313	1	1.7	386	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
314	1	1.7	314	1	1.7	387	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
315	1	1.7	315	1	1.7	388	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
316	1	1.7	316	1	1.7	389	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
317	1	1.7	317	1	1.7	390	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
318	1	1.7	318	1	1.7	391	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
319	1	1.7	319	1	1.7	392	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
320	1	1.7	320	1	1.7	393	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
321	1	1.7	321	1	1.7	394	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
322	1	1.7	322	1	1.7	395	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
323	1	1.7	323	1	1.7	396	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
324	1	1.7	324	1	1.7	397	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae
325	1	1.7	325	1	1.7	398	6	1.7	355	1	PSBA_VIGUN	Q43593	olea europae

399	1	1.7	414	1	COT2_HUMAN	P24468	homo sapien	472	1.7	502	1	CATA_PIG	O62839	sus scrofa
400	1	1.7	414	1	COT2_MOUSE	P43135	mus musculus	473	1.7	505	1	TCMO_CICAR	O81928	cicer ariet
401	1	1.7	414	1	COT2_RAT	O09018	rattus norv	474	1.7	506	1	CATA_BOVIN	P00432	bos taurus
402	1	1.7	414	1	CPTR_SOLTU	P29463	solanum tub	475	1.7	506	1	CATA_DRONE	P17336	drosophila
403	6	1.7	416	1	GLVA_HELPJ	O92mp7	helicobacte	476	1.7	507	1	IRX3_MOUSE	P81067	mus musculus
404	6	1.7	416	1	GLVA_HELPJ	P56089	helicobacte	477	1.7	507	1	MEFA_HUMAN	O02078	homo sapien
405	6	1.7	419	1	G6AC_DROME	P83295	drosophila	478	1.7	510	1	YOT3_CAEEL	P34649	caenorhabdi
406	6	1.7	420	1	O63A_DROME	O9vzw8	drosophila	479	1.7	511	1	COPD_BOVIN	P33619	bos taurus
407	6	1.7	420	1	PGKE_TRYBB	P08893	trypanosoma	480	1.7	511	1	COPD_HUMAN	P48444	homo sapien
408	6	1.7	420	1	PROA_NEIMA	O91uk8	neisseria m	481	1.7	513	1	WRK3_ARATH	O92q70	arabidopsis
409	6	1.7	420	1	PROA_NEIMA	O91zg3	neisseria m	482	1.7	513	1	GLCM_MOUSE	P17439	mus musculus
410	6	1.7	421	1	CC8_RAT	O8jhw5	rattus norv	483	1.7	516	1	EX7L_CHLTR	O84333	chlamydia t
411	6	1.7	421	1	FTSZ_HAFIN	P07377	trypanosoma	484	1.7	520	1	YNT3_MYCTU	O10508	mycobacteri
412	6	1.7	421	1	PK8B_TRYBB	P03660	bacterioph	485	1.7	522	1	LNT_HAEIN	P44626	haemophilus
413	6	1.7	422	1	VG2_BPIKE	O60632	mus musculus	486	1.7	524	1	VG20_BP74	P13334	bacterioph
414	6	1.7	422	1	COT1_MOUSE	O02031	homo sapien	487	1.7	526	1	CATA_BRARE	O9pt92	brachydanio
415	6	1.7	422	1	PSDB_HUMAN	P10589	homo sapien	488	1.7	526	1	CATA_CANFA	O97492	canis famli
416	6	1.7	423	1	COT1_HUMAN	O10589	homo sapien	489	1.7	526	1	CATA_MOUSE	P04040	homo sapien
417	6	1.7	424	1	COT1_BOVIN	O9ctr8	bos taurus	490	1.7	526	1	CATA_MOUSE	P24270	mus musculus
418	6	1.7	425	1	LMP2_CHICK	O90617	gallus gall	491	1.7	527	1	CATA_RAT	P04762	rattus norv
419	6	1.7	426	1	YF26_MYCTU	O50581	mycobacteri	492	1.7	527	1	CATA_RANRU	O9pwf7	rana rugosa
420	6	1.7	428	1	FAB2_MOUSE	O64733	mus musculus	493	1.7	527	1	HSF8_LYCES	O40152	lycopersico
421	6	1.7	430	1	NPX1_HUMAN	O15818	homo sapien	494	1.7	528	1	MASY_EMENI	P28344	emerlicella
422	6	1.7	433	1	FTSZ_ARATH	O42545	arabidopsis	495	1.7	528	1	V58K_BSMV	P04867	barley stri
423	6	1.7	433	1	HISX_ECOLI	P06988	escherichia	496	1.7	529	1	DHAL_ENTHI	P30840	entamoeba h
424	6	1.7	434	1	HEMI_PASNU	P95525	pasteurella	497	1.7	530	1	MATP_HUMAN	O9umx9	homo sapien
425	6	1.7	434	1	YHFT_ECOLI	P45546	escherichia	498	1.7	533	1	MASY_ECOLI	P08997	escherichia
426	6	1.7	435	1	EF1A_SULSO	P35021	sulfolobus	499	1.7	534	1	P4HI_MOUSE	O60715	mus musculus
427	6	1.7	436	1	EF1G_XENLA	P26642	xenopus lae	500	1.7	536	1	GLCM_MOUSE	P04052	homo sapien
428	6	1.7	436	1	SECY_METJA	O60175	methanococ	501	1.7	540	1	TOP1_AQUAE	O66893	aquifex aeo
429	6	1.7	437	1	E2F2_HUMAN	O14209	homo sapien	502	1.7	541	1	MASY_STRAL	O92h77	streptomyce
430	6	1.7	438	1	SECY_METVA	P28541	methanococ	503	1.7	542	1	ZYX_CHICK	O04584	gallus gall
431	6	1.7	439	1	GLNA_THEMEA	P36205	thermotoga	504	1.7	543	1	MASY_STRAE	P77947	streptomyce
432	6	1.7	440	1	PGKC_TRYBB	P07378	trypanosoma	505	1.7	546	1	MCP3_ECOLI	P05704	escherichia
433	6	1.7	442	1	FTSZ_CORGL	P94337	corynebacte	506	1.7	547	1	ODP2_PSEAE	O59638	pseudomonas
434	6	1.7	443	1	NRTA_SYNP7	P38043	synechococ	507	1.7	552	1	AAK2_HUMAN	P54646	homo sapien
435	6	1.7	446	1	NV5R_PIG	O37969	sus scrofa	508	1.7	553	1	AAK2_RAT	O09137	rattus norv
436	6	1.7	448	1	FIBP_ADEP3	O83457	porcine ade	509	1.7	553	1	NIFA_RHOCA	P09434	rhodobacter
437	6	1.7	450	1	HSLU_AQUAE	O66574	aquifex aeo	510	1.7	553	1	ODO2_MYCTU	O10381	mycobacteri
438	6	1.7	452	1	ERF1_TRYBB	O9nax8	trypanosoma	511	1.7	556	1	FTHS_CLOCY	O07064	clostridium
439	6	1.7	454	1	AEP_YARLI	P09230	yartocwia li	512	1.7	557	1	ACHI_SCHGR	P23414	schistoscer
440	6	1.7	454	1	IMDH_PNECA	O12658	pneumocysti	513	1.7	561	1	MASY_BRANA	P13244	brassica na
441	6	1.7	456	1	SECY_METTH	O26134	nethanobact	514	1.7	563	1	SYR_STRPN	O54869	streptococ
442	6	1.7	459	1	COBG_PSEDE	P21637	pseudomonas	515	1.7	564	1	ZYX_MOUSE	O62523	mus musculus
443	6	1.7	461	1	NRH2_HUMAN	P55035	homo sapien	516	1.7	566	1	GUNE_PAEIA	P23350	paenibacill
444	6	1.7	462	1	A2AC_HUMAN	P18825	homo sapien	517	1.7	566	1	MASY_CUCMA	P24571	cucurbita m
445	6	1.7	462	1	ENGA_ENTAE	O59342	enterobacte	518	1.7	566	1	MASY_RAPSA	O43827	raphanus sa
446	6	1.7	463	1	ENGA_MYCTU	O33212	mycobacteri	519	1.7	567	1	MASY_GOSHI	P17432	gossypium h
447	6	1.7	464	1	GSA_CHLRE	P19969	chlamydomon	520	1.7	568	1	CH60_BUGGR	O08216	cucumisa gra
448	6	1.7	464	1	GAA5_RAT	P22165	rhesus papl	521	1.7	569	1	C972_SOYBN	O39727	euglena gra
449	6	1.7	466	1	VL2_RHPV1	O61398	mus musculus	522	1.7	576	1	CC18_SCHPO	O48921	glycine max
450	6	1.7	468	1	PCOI_MOUSE	O08628	rattus norv	523	1.7	577	1	POF3_SCHPO	P43411	schizosacch
451	6	1.7	468	1	PCOI_MOUSE	P57074	gallus gall	524	1.7	583	1	FTSZ_AGRTO	O30992	agrobacteri
452	6	1.7	470	1	SOXB_CHICK	O53304	mycobacteri	525	1.7	584	1	RECN_SYNX3	P74374	synechocyst
453	6	1.7	472	1	YU87_MYCTU	P06414	marchantia	526	1.7	585	1	DHSA_BACSU	P08065	bacillus su
454	6	1.7	473	1	PSBC_MARPO	O984x8	rhizobium l	527	1.7	591	1	DAK2_YEAST	P43550	saccharomyc
455	6	1.7	477	1	SYC_RHIL0	O9nms5	homo sapien	528	1.7	592	1	FTSZ_BARBA	O31314	bartonella
456	6	1.7	478	1	GSR2_HUMAN	P04004	homo sapien	529	1.7	600	1	DNAX_EYRBA	O05647	erysipeloth
457	6	1.7	478	1	YVNC_HUMAN	P33369	escherichia	530	1.7	601	1	DEAD_BUCAL	P57453	buchnera ap
458	6	1.7	478	1	YONG_ECOLI	P42437	escherichia	531	1.7	604	1	CIOI_MOUSE	P97414	mus musculus
459	6	1.7	483	1	NASF_BACSU	O43415	capsicum an	532	1.7	606	1	MM17_HUMAN	O9u129	homo sapien
460	6	1.7	484	1	IRX5_MOUSE	O791kq4	mus musculus	533	1.7	608	1	UGST_ANTWA	O82627	antirrhinum
461	6	1.7	488	1	DGT1_HUMAN	O75907	homo sapien	534	1.7	609	1	REAL_XENLA	O01588	xenopus lae
462	6	1.7	488	1	MM11_HUMAN	P24347	homo sapien	535	1.7	614	1	ODP2_HUMAN	P05151	h dihydrol
463	6	1.7	490	1	MOT3_YEAST	P47785	saccharomyc	536	1.7	614	1	YHQX_ECOLI	P33353	escherichia
464	6	1.7	491	1	DG1L_CERAE	O9gmf1	cercopithe	537	1.7	615	1	MUTA_MYCTU	P71773	mycobacteri
465	6	1.7	498	1	LCVB_CAPAN	O43415	capsicum an	538	1.7	616	1	YGF_HUMAN	O15240	homo sapien
466	6	1.7	498	1	MEFA_MOUSE	O60929	mus musculus	539	1.7	617	1	CYG2_HUMAN	O75343	homo sapien
467	6	1.7	498	1	YAOI_SCHPO	O10097	schizosacch	540	1.7	618	1	DNAX_STRCO	O05558	streptomyce
468	6	1.7	500	1	LCVB_LYCES	O43503	lycopersico	541	1.7	618	1	DNAX_STRGR	O34215	streptomyce
469	6	1.7	500	1	LCVB_TOBAC	O43578	nicotiana t	542	1.7	621	1	GIDA_BORBU	P33362	borrelia bu
470	6	1.7	500	1	US24_HCMVA	P09700	human cytom	543	1.7	621	1	HCY6_ANDAU	P80476	androctonus
471	6	1.7	501	1	XYLB_LACPE	P21939	lactobacill	544	1.7	626	1			

545	1	1.7	626	Q92bq5	listeria in	618	1	917	1	HXA3_HAEIN	P45355	haemophilus
546	1	1.7	626	P47762	listeria mo	619	1	919	1	DNL1_HUMAN	P18858	homo sapien
547	1	1.7	630	P23799	trypanosoma	620	1	928	1	HXA2_HAEIN	P45354	haemophilus
548	1	1.7	630	P26337	trypanosoma	621	1	929	1	CAIC_NOTVI	Q91145	notophthalin
549	6	1.7	633	P08150	escherichia	622	1	933	1	SLAP_CAMPE	P35827	campylobact
550	6	1.7	635	P45796	paenibacilli	623	1	952	1	YK15_CAEEL	P46012	caenorhabdi
551	6	1.7	637	P10802	azotobacter	624	1	954	1	XYNA_RUMPL	P29126	ruminococcu
552	6	1.7	641	Q9sin4	streptomyce	625	1	961	1	TSP4_HUMAN	P35443	homo sapien
553	6	1.7	644	P07130	bacillus th	626	1	968	1	SNXD_HUMAN	Q9y5w8	homo sapien
554	6	1.7	646	Q9nzul	homo sapien	627	1	970	1	SECA_CHLPN	Q9y5w8	homo sapien
555	6	1.7	646	P38688	saccharomyc	628	1	974	1	RHG6_HUMAN	O43182	chlamydia p
556	6	1.7	647	P44135	haemophilus	629	1	978	1	PEX6_RAT	P54777	rattus norv
557	6	1.7	648	Q9vku7	drosophila	630	1	1005	1	GCP_CAEEL	Q10663	caenorhabdi
558	6	1.7	649	Q45744	bacillus th	631	1	1013	1	PTPX_MACNE	O02695	macaca neme
559	6	1.7	651	P40357	saccharomyc	632	1	1018	1	HMW1_MYCPN	Q50365	mycoplasma
560	6	1.7	652	Q06117	bacillus th	633	1	1030	1	Y075_MYCPN	P75556	mycoplasma
561	6	1.7	652	Q51705	paracoccus	634	1	1048	1	CPXB_BACME	P14779	bacillus me
562	6	1.7	656	Q10687	mycobacteri	635	1	1048	1	P100_HCMVA	O8u085	human cytom
563	6	1.7	670	P33792	rattus norv	636	1	1056	1	CARB_PYRFU	P08318	human cytom
564	6	1.7	672	P31639	homo sapien	637	1	1060	1	2PH1_DROME	P28166	pyrococcus
565	6	1.7	675	Q54828	mus musculu	638	1	1088	1	DP0D_SOYBN	Q8y9s3	herpesvirus
566	6	1.7	677	P49805	mus musculu	639	1	1125	1	S24C_HUMAN	Q9y9s2	herpesvirus
567	6	1.7	682	P22717	rattus norv	640	1	1127	1	TFIG_HUMAN	Q9qzm6	rattus norv
568	6	1.7	684	P50273	saccharomyc	641	1	1142	1	SPK_HUMAN	Q9npq4	homo sapien
569	6	1.7	692	Q43823	homo sapien	642	1	1147	1	SRE1_HUMAN	Q9npq3	homo sapien
570	6	1.7	692	O17020	anopheles g	643	1	1169	1	C8BA_BACUK	Q92797	homo sapien
571	6	1.7	693	Q9cmb4	pasteurella	644	1	1171	1	DPOL_HSVT1	P36956	homo sapien
572	6	1.7	693	O14286	schizosacch	645	1	1171	1	DPOL_HSVT1	O45705	bacillus th
573	6	1.7	695	O54479	caulobacter	646	1	1181	1	PKX1_RAT	Q9y9s3	herpesvirus
574	6	1.7	699	P20166	bacillus su	647	1	1184	1	PC12_HUMAN	Q9y9s2	herpesvirus
575	6	1.7	701	P57444	buchnera ap	648	1	1184	1	RTN4_HUMAN	Q9npq4	homo sapien
576	6	1.7	704	Q02038	su scrofa	649	1	1192	1	K125_CAEEL	Q9npq3	homo sapien
577	6	1.7	704	P45846	drosophila	650	1	1223	1	CTD2_HUMAN	O10925	caenorhabdi
578	6	1.7	705	O88022	streptomyce	651	1	1229	1	N121_HUMAN	Q9ugb3	homo sapien
579	6	1.7	706	Q9qxs6	mus musculu	652	1	1233	1	NME3_HUMAN	Q9y2n3	homo sapien
580	6	1.7	713	P20239	mus musculu	653	1	1237	1	NME3_RAT	Q14957	homo sapien
581	6	1.7	713	ERF2_CANAL	ERF2_CANAL	654	1	1239	1	NARG_MOUSE	Q10998	mus musculu
582	6	1.7	716	PBPB_BACSU	Q13354	654	1	1246	1	NARG_ECOLI	P09152	escherichia
583	6	1.7	717	PBPB_HUMAN	Q07868	655	1	1247	1	CTD2_MOUSE	O35927	mus musculu
584	6	1.7	722	Q9h4q3	homo sapien	656	1	1274	1	BXF_CLOBO	P30996	clostridium
585	6	1.7	730	P7768	haemophilus	657	1	1295	1	GLP1_CAEEL	P13508	caenorhabdi
586	6	1.7	735	P34115	dictyosteli	658	1	1332	1	XKDO_BACSU	P43334	bacillus su
587	6	1.7	735	P36009	saccharomyc	659	1	1361	1	YME5_YEAST	Q04693	saccharomyc
588	6	1.7	741	Q63531	rattus norv	660	1	1381	1	CTAI_RAT	P97846	rattus norv
589	6	1.7	742	P28468	halocynthia	661	1	1384	1	CTAI_HUMAN	P78357	homo sapien
590	6	1.7	750	O15119	homo sapien	662	1	1399	1	L112_CAEEL	Q9bv12	homo sapien
591	6	1.7	758	P96256	mycobacteri	663	1	1429	1	VE65_HSVI1	P14585	caenorhabdi
592	6	1.7	758	Q52880	rhizobium m	664	1	1434	1	IE18_PVKVA	Q00106	ictaluriid h
593	6	1.7	760	P57142	buchnera ap	665	1	1461	1	IE18_PVKVA	P33479	pseudorabie
594	6	1.7	763	O05564	mycobacteri	666	1	1463	1	DPO3_STRPN	P11675	pseudorabie
595	6	1.7	763	P32479	saccharomyc	667	1	1463	1	NME1_HUMAN	Q978q2	streptococ
596	6	1.7	788	Q9epw9	mus musculu	668	1	1464	1	NME1_MOUSE	Q12879	homo sapien
597	6	1.7	795	P25644	saccharomyc	669	1	1464	1	NME1_MOUSE	P35436	mus musculu
598	6	1.7	803	Q45755	bacillus th	670	1	1464	1	NME1_MOUSE	Q00959	rattus norv
599	6	1.7	804	P09959	saccharomyc	671	1	1465	1	DPO3_STRPN	Q9dfi9	streptococ
600	6	1.7	804	P17922	bacillus su	672	1	1509	1	GSRI_HUMAN	Q9nzm4	homo sapien
601	6	1.7	808	Q04883	pimpinella	673	1	1520	1	ABL_DROME	P00522	drosophila
602	6	1.7	808	Q41142	ricinus com	674	1	1569	1	YPJA_ECOLI	P52143	escherichia
603	6	1.7	808	P33400	nicotiana t	675	1	1574	1	MY52_YEAST	P19524	saccharomyc
604	6	1.7	809	O04855	vigna ungu	676	1	1582	1	YU30_RALSO	O8xv02	raistonia s
605	6	1.7	822	Q12929	homo sapien	677	1	1582	1	41_DROME	Q9v8r9	drosophila
606	6	1.7	823	P14907	saccharomyc	678	1	1723	1	PM20_CHLPN	Q92b12	chlamydia p
607	6	1.7	824	Q9udy8	homo sapien	679	1	1772	1	MSPI_PLAYO	P13828	plasmodium
608	6	1.7	824	P53532	corynebacte	680	1	1804	1	YFA7_YEAST	P43583	saccharomyc
609	6	1.7	824	Q9hcx4	homo sapien	681	1	1812	1	SUIS_SUNMU	O62653	suncus mui
610	6	1.7	862	Q9wvc5	mus musculu	682	1	1815	1	SHK3_RAT	Q911u4	rattus norv
611	6	1.7	865	Q02910	drosophila	683	1	1849	1	FAS2_SCHPO	Q10289	s fatty aci
612	6	1.7	873	P40309	saccharomyc	684	1	1849	1	BIG1_BOVIN	O46382	bos taurus
613	6	1.7	876	Q9wvc5	mus musculu	685	1	1849	1	BIG1_BOVIN	Q9y6d6	homo sapien
614	6	1.7	880	P33953	saccharomyc	686	1	1849	1	BIG1_BOVIN	Q9y6d6	homo sapien
615	6	1.7	884	P34459	caenorhabdi	687	1	1885	1	FAS2_CANAL	P43098	c fatty aci
616	6	1.7	894	Q12906	h interleuk	688	1	2026	1	CYAA_YEAST	P08678	saccharomyc
617	6	1.7	895	Q3886	rattus norv	689	1	2035	1	Y233_HUMAN	Q92508	homo sapien
	6	1.7	902	O75891	homo sapien	690	1	2116	1	RRPL_SYN	P31332	sonchus yel

691	1.7	2144	1	GLT1_YEAST	Q12680	saccharomyc	764	1.5	73	1	HL4_RABIT	P02552	oryctolagus
692	1.7	2298	1	CU05_HUMAN	Q9Y3X5	homo sapien	765	1.5	74	1	RPOZ_HELPY	P25467	helicobacte
693	1.7	2332	1	POLG_FMDVA	P03308	f genome po	766	1.5	75	1	COXH_HUMAN	P09669	homo sapien
694	1.7	2332	1	POLG_FMDVA	P03308	f genome po	767	1.5	75	1	HMSA_SALSA	P09636	salmo salar
695	1.7	2333	1	POLG_FMDV1	P03306	f genome po	768	1.5	75	1	HOLI_BPRIT	Q38134	bacterioph
696	1.7	2504	1	FAS_HUMAN	P49327	homo sapien	769	1.5	75	1	RS21_BRUME	Q8Y445	brucella me
697	1.7	2505	1	FAS_RAT	P12785	rattus norv	770	1.5	75	1	Y261_BACHD	Q9K952	baecillus ha
698	1.7	2766	1	THYG_MOUSE	O08710	mus musculus	771	1.5	76	1	TXP6_APTSC	P49700	apostichus
699	1.7	2768	1	THYG_HUMAN	P01266	homo sapien	772	1.5	76	1	UBIQ_COPCO	P19848	coprinus co
700	1.7	3053	1	CAIC_HUMAN	P06882	rattus norv	773	1.5	76	1	UBIQ_SOYBN	P03993	glycine max
701	1.7	3058	1	CAIC_HUMAN	Q99715	homo sapien	774	1.5	76	1	UL79_HSV62	P25448	human herpe
702	1.7	3058	1	POLG_PEMVC	Q01500	p genome po	775	1.5	76	1	UL79_HSV62	O29163	archaeoglob
703	1.7	3119	1	CAIC_MOUSE	Q06047	mus musculus	776	1.5	77	1	GEPB_BACSU	O06720	baecillus su
704	1.7	3206	1	POLG_PSBMV	P29152	p genome po	777	1.5	77	1	RL28_ECOLI	P02428	escherichia
705	1.7	3567	1	ERY2_SACER	Q03132	saccharopol	778	1.5	77	1	RL28_SALTY	O54325	salmonella
706	1.7	3674	1	SPCR_HUMAN	Q9NRC6	homo sapien	779	1.5	77	1	YGRG_BACFI	Q45132	baecillus fi
707	1.7	4273	1	PKSM_BACSU	P08882	rattus norv	780	1.5	78	1	CINA_STRGV	P29827	streptover
708	1.7	4499	1	DYHA_CHLRE	Q39610	chlamydomon	781	1.5	78	1	RL28_PSEAE	Q9HNT8	pseudomonas
709	1.7	5217	1	HTSI_COCCA	Q01886	cochliobolu	782	1.5	79	1	CSMA_CHLAU	P09928	chloroflexu
710	1.5	14	1	UHA1_CANFA	P99503	canis famli	783	1.5	79	1	NSGX_HUMAN	Q9UH64	homo sapien
711	1.5	14	1	UHA1_CANFA	P99503	canis famli	784	1.5	79	1	POC1_BRARA	O42470	brassica ra
712	1.5	15	1	UN46_CLOPA	P81362	clostridium	785	1.5	79	1	PSBH_CHLVU	P56323	chlorella v
713	1.5	15	1	LEC2_PSOSC	P22585	psophocarpu	786	1.5	79	1	YKEF_ECOLI	P75677	escherichia
714	1.5	15	1	PLAS_MICAE	P10625	microcystis	787	1.5	80	1	PYSL_ANASP	P07124	anabaena sp
715	1.5	20	1	CD4_SHEEP	P05342	ovis aries	788	1.5	82	1	CEP_VIBCH	Q9K323	vibrio chol
716	1.5	22	1	ANFC_CHICK	P21805	gallus gall	789	1.5	82	1	CX7_NAJAT	P49122	naja atra
717	1.5	23	1	AU42_LITRA	P82398	litoria ran	790	1.5	82	1	CX72_NAJAT	O10359	oryzla pseu
718	1.5	27	1	ANF_ANGJA	P18144	anguilla ja	791	1.5	83	1	CX7P_NAJAT	Q91126	naja atra
719	1.5	27	1	IPPD_MOUSE	Q06029	mus musculus	792	1.5	83	1	CX7A_NAJAT	O19996	naja atra
720	1.5	28	1	PA2C_PSEPO	P20260	pseudechis	793	1.5	83	1	CX7A_NAJAT	Q91126	naja atra
721	1.5	30	1	UP61_UPEIN	P82037	uperoleia i	794	1.5	83	1	CX7A_NAJAT	Q91126	naja atra
722	1.5	30	1	UP62_UPEIN	P82038	uperoleia i	795	1.5	83	1	POC1_ARATH	Q98P7	arabidopsi
723	1.5	35	1	VORB_METTM	P80908	methanobact	796	1.5	83	1	POC2_ARATH	Q91F54	arabidopsi
724	1.5	36	1	ANFV_ANGJA	P22642	anguilla ja	797	1.5	84	1	POC2_BRARA	Q39406	brassica ra
725	1.5	36	1	RL6_HALCU	P05968	halobacteri	798	1.5	84	1	EX7S_HAEIN	P43914	haemophilus
726	1.5	37	1	PSAJ_EUGGR	P30394	euglena gra	799	1.5	84	1	OAG1_SALTY	Q03032	salmonella
727	1.5	40	1	RRO_LSV	P27328	lily sympto	800	1.5	85	1	YPB3_ECOLI	P03851	escherichia
728	1.5	44	1	COAT_BPPE3	Q9X715	prochloropha	801	1.5	85	1	POC4_ALNGL	Q81701	aliquis gluti
729	1.5	44	1	PSAJ_PROMA	P80359	hevea bras	802	1.5	85	1	POC4_BEVE	Q39419	betula verr
730	1.5	45	1	HEVP_HEVER	P09542	mus musculus	803	1.5	85	1	PYS1_FREDI	P11377	fremyella d
731	1.5	46	1	CSPA_KLEPN	P01078	solanum mel	804	1.5	85	1	Y12_BPT7	Q03780	bacterioph
732	1.5	47	1	RL32_HELPJ	Q48493	klebsiella	805	1.5	85	1	YCFR_ECOLI	P75953	escherichia
733	1.5	47	1	RL32_HELPJ	Q48493	klebsiella	806	1.5	85	1	YML5_PASTE	P15616	paramecium
734	1.5	50	1	PRVM_SCVCA	P56054	helicobacte	807	1.5	87	1	YB21_CAUCR	Q9A387	caulobacter
735	1.5	51	1	MLEV_MOUSE	P35491	scyllorhinu	808	1.5	87	1	YBED_ECOLI	P30977	escherichia
736	1.5	52	1	IPR_SOLME	P09542	mus musculus	809	1.5	88	1	APC1_CANFA	P56595	canis famli
737	1.5	52	1	RUBR_TREPA	P01078	solanum mel	810	1.5	88	1	APC1_MOUSE	P34928	mus musculu
738	1.5	52	1	YABO_ECOLI	O83956	treponema p	811	1.5	88	1	APC1_RAT	P19939	rattus norv
739	1.5	55	1	PHNS_DESVH	P39221	escherichia	812	1.5	88	1	GP42_BPSPI	O48398	bacterioph
740	1.5	56	1	H2AQ_HUMAN	Q06173	desulfovibr	813	1.5	88	1	H2A3_STRPU	P09530	strongyloce
741	1.5	57	1	HPIS_RHOGL	Q16777	homo sapien	814	1.5	88	1	RL37_CANAL	Q9P836	candida alb
742	1.5	60	1	HXB2_SALSA	P38589	rhodopila g	815	1.5	88	1	RS21_RHILO	O989Y4	rhizobium l
743	1.5	61	1	PPSA_ERWHE	P09638	salmo salar	816	1.5	88	1	VHED_BPIKE	P03670	bacterioph
744	1.5	62	1	CXH_NAJKA	O54457	erwinia her	817	1.5	88	1	Y874_CAUCR	P58091	caulobacter
745	1.5	62	1	SCX6_TITSE	P14541	naja naja k	818	1.5	89	1	YAYD_SCHPO	O10220	schizosacch
746	1.5	63	1	ANPL_AUSBR	P45669	tityus serr	819	1.5	90	1	NTPI_SPVKA	Q08513	swinepox vi
747	1.5	63	1	ANP2_AUSBR	P12100	australycic	820	1.5	90	1	HXA2_NOTVI	P31261	notophthalm
748	1.5	64	1	YRKO_BACSU	P12101	australycic	821	1.5	90	1	Y169_RICPR	Q92424	rickettsia
749	1.5	64	1	SAS4_BACSU	P04833	baecillus su	822	1.5	90	1	Y215_RICPR	Q924V4	rickettsia
750	1.5	65	1	LHA3_RHOPA	P35103	rhodopsu	823	1.5	91	1	VPJ1_ECOLI	P58095	escherichia
751	1.5	65	1	YP7A_TNVD	P27211	tobacco nec	824	1.5	91	1	VG76_BPM5	P58095	escherichia
752	1.5	66	1	LHA2_RHOPA	P35102	rhodopsu	825	1.5	92	1	NODE_RHILV	Q05291	mycobacteri
753	1.5	68	1	CYC3_DESAC	P00137	desulfofuro	826	1.5	92	1	VGL1_HSV11	P04680	herpes simp
754	1.5	68	1	PLEX_PSEAM	Q9PRJ9	pseudopleur	827	1.5	92	1	Y886_METTH	O26972	methanobact
755	1.5	68	1	VHTJ_LAMBD	P03727	bacterioph	828	1.5	93	1	YSV3_CAEEL	Q10009	caenorhabdi
756	1.5	68	1	YLK5_CAEEL	P41953	caenorhabdi	829	1.5	93	1	REPI_ECOLI	P05830	escherichia
757	1.5	69	1	MOP_HAEIN	P45183	haemophilus	830	1.5	94	1	YQIC_CAEEL	Q09283	caenorhabdi
758	1.5	70	1	CSPI_ECOLI	P77605	escherichia	831	1.5	94	1	ASR1_YERPE	Q82665	yersinia pe
759	1.5	70	1	CSPI_SALTI	P58726	salmonella	832	1.5	95	1	ESA6_MYCTU	Q57165	mycobacteri
760	1.5	70	1	CSPI_SALTI	P39818	salmonella	833	1.5	96	1	YFI_ORYSA	O23810	oryza sativ
761	1.5	70	1	RS21_CAMJE	Q9PID2	campylobact	834	1.5	96	1	ABRB_BACSU	P08874	baecillus su
762	1.5	71	1	SAS1_BACCE	P06351	baecillus ce	835	1.5	96	1	PRGB_HUMAN	Q02325	homo sapien
763	1.5	71	1	MBTH_MYCTU	O05821	mycobacteri	836	1.5	97	1	RL15_STRSC	P43415	streptomyce
				V07K_PVXHB	Q07631	potato viru					FER2_CVACA	P15789	cyenidium c

837	1	1.5	97	1	KEFL_ECOLI	Q52281	escherichia
838	1	1.5	97	1	NUCC_SOYBN	P31174	glycine max
839	1	1.5	98	1	FIS_FASHA	O54367	pasteurella
840	1	1.5	98	1	MOBS_THIFE	P20086	thiobacillus
841	1	1.5	98	1	RS20_CHLMU	O9pj64	chlamydia m
842	1	1.5	98	1	VHED_BPPLH	O07481	bacterioph
843	1	1.5	99	1	NIC1_HUMAN	O9ug19	homo sapien
844	1	1.5	99	1	PLAS_CUCPE	P00292	curcurbita p
845	1	1.5	99	1	RS20_CHLPN	O927f2	chlamydia p
846	1	1.5	99	1	Z233_MCEGE	P47475	mycoplasma
847	1	1.5	100	1	Y837_NEIMB	Q91225	neisseria m
848	1	1.5	100	1	YKPB_YEAST	P36055	saccharomyc
849	1	1.5	101	1	RS14_RHIME	Q92qf7	rhizobium m
850	1	1.5	101	1	YG75_MYCPE	P75117	mycoplasma
851	1	1.5	102	1	ARSC_NEIGO	P53534	neisseria g
852	1	1.5	102	1	FLAF_CAUCR	P21295	caulobacter
853	1	1.5	102	1	GLRX_RICCO	P55143	ricinus com
854	1	1.5	102	1	SECG_STRCO	Q92521	streptomyce
855	1	1.5	102	1	TXOB_HADIN	Q9bjw0	hadronyche
856	1	1.5	102	1	Y224_METTH	O26326	methanobact
857	1	1.5	103	1	ANFB_BOVIN	P13204	bos taurus
858	1	1.5	103	1	CHLB_NEPEX	P37850	nephrolepis
859	1	1.5	103	1	RL21_HAEIN	P44359	haemophilus
860	1	1.5	103	1	TCTA_HUMAN	P57738	homo sapien
861	1	1.5	103	1	YA46_NEIMA	Q9jv14	neisseria m
862	1	1.5	103	1	YB84_MYCPL	P75301	mycoplasma
863	1	1.5	103	1	YGBQ_ECOLI	Q46894	escherichia
864	1	1.5	104	1	KAC6_RABIT	P03984	oryctolagus
865	1	1.5	104	1	LAC2_MOUSE	P01844	mus musculus
866	1	1.5	104	1	LAC2_RAT	P20767	rattus norv
867	1	1.5	104	1	LAC3_MOUSE	P01845	mus musculus
868	1	1.5	104	1	Y4EB_RHISN	P55425	rhizobium s
869	1	1.5	105	1	HXB4_BRARE	P22574	brachydanio
870	1	1.5	105	1	INS_SHEEP	P01318	ovis aries
871	1	1.5	105	1	LAC1_MOUSE	P01843	mus musculus
872	1	1.5	105	1	LAC_HUMAN	P01846	homo sapien
873	1	1.5	105	1	LAC_PIG	P01847	sus scrofa
874	1	1.5	105	1	LAC_RABIT	P01847	oryctolagus
875	1	1.5	105	1	YOPN_BACSU	Q34369	bacillus su
876	1	1.5	106	1	ATPR_DROME	Q24707	drosophila
877	1	1.5	106	1	RL12_ARCFU	O28780	archaeoglob
878	1	1.5	106	1	THIO_SFPAU	P33791	streptomyce
879	1	1.5	106	1	VHSE_BPT3	P20322	bacterioph
880	1	1.5	106	1	YBHO_YEAST	P38186	saccharomyc
881	1	1.5	107	1	CYC_APIME	P00341	homo sapien
882	1	1.5	107	1	GRO_HUMAN	O8ye38	brucella me
883	1	1.5	107	1	HIS2_BRUME	O74948	schizosacch
884	1	1.5	107	1	T2AG_SCHPO	P06590	murine coro
885	1	1.5	107	1	VNS2_CVMJH	Q9ckf3	pasteurella
886	1	1.5	107	1	YG68_PASMU	P00030	eisenia foe
887	1	1.5	108	1	CYC_EISFO	P01315	sus scrofa
888	1	1.5	108	1	INS_PIG	Q46560	bacteroides
889	1	1.5	108	1	VAPI_BACNO	Q9zcd1	rickettsia
890	1	1.5	108	1	Y826_RICPR	O8xwk9	ralstonia s
891	1	1.5	108	1	Y065_RALSO	P00041	issatchenki
892	1	1.5	109	1	CYC_ISSOR	Q9mvv9	bos taurus
893	1	1.5	109	1	TRP5_BOVIN	P41420	autographa
894	1	1.5	109	1	Y005_NPVAN	P57825	pasteurella
895	1	1.5	109	1	Y205_PASMU	P17577	escherichia
896	1	1.5	109	1	YBAB_ECOLI	P58622	homo sapien
897	1	1.5	110	1	Y208_LISMO	P26541	human papil
898	1	1.5	110	1	VL3_HPVS5B	P33382	listeria mo
899	1	1.5	110	1	YK21_CAEEL	O8z96	yersinia pe
900	1	1.5	110	1	YV21_YERPE	Q9j3w9	aeropyrum p
901	1	1.5	111	1	RL12_AERPE	P14626	rana catesb
902	1	1.5	111	1	RNPL_RANCA	Q55397	synecocyst
903	1	1.5	111	1	Y546_SYNY3	O32262	bacillus su
904	1	1.5	111	1	YVDS_BACSU	P03673	bacterioph
905	1	1.5	111	1	COAD_BPFD	O54053	rhizobium e
906	1	1.5	112	1	GLNB_RHET	P13556	rhodobacter
907	1	1.5	112	1	GLNB_RHOA	P09589	lytechinus
908	1	1.5	112	1	H2A3_LYTP1		

910	1	1.5	112	1	KV2A_MOUSE	P01626	mus musculus
911	1	1.5	112	1	KV2D_MOUSE	P01629	mus musculus
912	1	1.5	112	1	PEDB_PEDAC	P36496	padlococcus
913	1	1.5	112	1	RBFA_MYGGE	P47389	mycoplasma
914	1	1.5	112	1	TGF2_BOVIN	P21214	bos taurus
915	1	1.5	112	1	YBAV_HAEIN	Q57134	haemophilus
916	1	1.5	112	1	FLIT_BACSU	P39740	bacillus su
917	1	1.5	113	1	KV2E_MOUSE	P03976	mus musculus
918	1	1.5	113	1	MEAL_PIG	Q95313	sus scrofa
919	1	1.5	113	1	RL12_HALVO	P41197	halobacteri
920	1	1.5	113	1	SSIF_STRBI	Q9r645	streptomyce
921	1	1.5	113	1	Y109_HAEIN	P43943	haemophilus
922	1	1.5	115	1	ACPM_MYCLE	O69475	mycobacteri
923	1	1.5	115	1	ACPM_MYCTU	Q10500	mycobacteri
924	1	1.5	115	1	SFP3_BOVIN	P04557	bos taurus
925	1	1.5	116	1	FLHD_PROMI	O34201	proteus mir
926	1	1.5	116	1	NU3M_MYTED	Q00568	mytilus edu
927	1	1.5	116	1	Y998_RHIME	P15550	strongyloce
928	1	1.5	116	1	ARSC_NEIMA	Q52966	rhizobium m
929	1	1.5	117	1	HV04_MOUSE	O9jqw0	neisseria m
930	1	1.5	117	1	WNT6_PLEJO	P01748	mus musculus
931	1	1.5	117	1	YFB9_YEAST	P28137	plethodon j
932	1	1.5	117	1	GLBN_NOSCO	P43576	saccharomyc
933	1	1.5	118	1	FLHD_YEREN	Q00812	nostoc comm
934	1	1.5	119	1	H2A4_PSAHI	O86046	yersinia en
935	1	1.5	119	1	LAMR_PETMA	P07793	psammehinu
936	1	1.5	119	1	PA21_NAJOX	P33577	petromyzon
937	1	1.5	119	1	RL17_BACSU	P25498	naja oxiana
938	1	1.5	119	1	YD52_PASMU	P20277	bacillus su
939	1	1.5	119	1	HPK_PSEPU	O5cl88	pasturella
940	1	1.5	120	1	INH_ERWCH	O87790	pseudomonas
941	1	1.5	120	1	KV2B_MOUSE	P18938	erwinia chr
942	1	1.5	120	1	PHS_YEAST	P01627	mus musculus
943	1	1.5	120	1	R18E_AERPE	P38744	saccharomyc
944	1	1.5	120	1	RBFA_CAMJE	Q9ybs1	aeropyrum p
945	1	1.5	120	1	RS20_DROME	O9pi20	campylobact
946	1	1.5	120	1	Y069_ARCFU	P55838	drosophila
947	1	1.5	120	1	YUTM_BACSU	O30167	archaeoglob
948	1	1.5	120	1	ACPS_BACSU	O32113	bacillus su
949	1	1.5	121	1	ANFB_MOUSE	P96618	bacillus su
950	1	1.5	121	1	H2B_PATGR	P40753	mus musculus
951	1	1.5	121	1	RK22_GUTH	P02284	patella gra
952	1	1.5	121	1	DBH_DEIRA	O46899	guillardia
953	1	1.5	122	1	FMNB_DESYM	Q9r289	deinococcus
954	1	1.5	122	1	H2B1_PSAHI	Q46604	desulfovibr
955	1	1.5	122	1	H2B_CAEEL	P02287	psammehinu
956	1	1.5	122	1	NRF1_SCHPO	P04255	caenorhabdi
957	1	1.5	122	1	RL7_BACST	Q9ur17	schizosacch
958	1	1.5	122	1	SMTE_SYNP7	P05392	bacillus st
959	1	1.5	122	1	YF94_MYCPN	P30340	synecococc
960	1	1.5	122	1	H2A_DROME	P75191	mycoplasma
961	1	1.5	123	1	H2A_PARLI	P02267	drosophila
962	1	1.5	123	1	H2A_PLADU	P13630	paracentrot
963	1	1.5	123	1	H2A_SIPNU	P19178	platynereis
964	1	1.5	123	1	H2A_STRPU	P02270	sipunculus
965	1	1.5	123	1	PA21_AKPI	P02271	strongyloce
966	1	1.5	123	1	YNIA_KLEPN	P51972	agkistrodon
967	1	1.5	123	1	FKBP_STRCH	P46382	klebsiella
968	1	1.5	124	1	H2A_ACRFO	P28725	streptomyce
969	1	1.5	124	1	H2A_ASTRU	P35061	acropora fo
970	1	1.5	124	1	H2A_SEPOF	P02269	asterias ru
971	1	1.5	124	1	H2A_URECA	P02268	septa offic
972	1	1.5	124	1	H2B_CHITH	P27325	urechis cau
973	1	1.5	124	1	NO5_VICSA	P21897	chironomus
974	1	1.5	124	1	YABJ_BACSU	O41705	vicia sativ
975	1	1.5	124	1	YC69_MYCTU	P37552	bacillus su
976	1	1.5	125	1	H2A3_PSAHI	Q11050	mycobacteri
977	1	1.5	125	1	H2AL_STRPU	P02265	psammehinu
978	1	1.5	125	1	LYC1_TACAC	P16886	strongyloce
979	1	1.5	125	1	PCDS_HUMAN	P37156	tachyglossu
980	1	1.5	125	1	PFDB_HALN1	O14737	homo sapien
981	1	1.5	125	1	PLAS_SYNP7	Q9Hsh0	halobacteri
982	1	1.5	125	1		P55020	synecococc


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RX MEDLINE-84108348; PubMed-6363059;
RA Braun G., Cole S.T.;
RT "Molecular characterization of the gene coding for major outer
RT membrane protein Ompa from Enterobacter aerogenes.";
RL Eur. J. Biochem. 137:495-500(1983).
CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
CC SOLUTES (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
CC
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DR EMBL: X00254; CAA25062.1;
DR PIR: S07222; S07222.
DR HSP; P02934; IQJP.
DR InterPro: IPR001145; Bac_OmpA.
DR Pfam: PF00691; OmpA; 1.
DR PRINTS: PR01021; OmpA_membrane; 1.
DR PRODOM: PD000930; Bac_OmpA; 1.
DR PROSITE: PS01068; OmpA; 1.
KW Outer membrane; Transmembrane; Phage recognition; Signal; Repeat;
KW Porin.
FT SIGNAL 1 21
FT CHAIN 22 350 OUTER MEMBRANE PROTEIN A.
FT TRANSMEM 27 40 POTENTIAL.
FT TRANSMEM 59 71 POTENTIAL.
FT TRANSMEM 74 89 POTENTIAL.
FT TRANSMEM 101 111 POTENTIAL.
FT TRANSMEM 115 130 POTENTIAL.
FT TRANSMEM 145 157 POTENTIAL.
FT TRANSMEM 163 179 POTENTIAL.
FT TRANSMEM 185 196 POTENTIAL.
FT DOMAIN 205 212 1.
FT REPEAT 205 206 4 X 2 AA TANDEM REPEATS OF A-P.
FT REPEAT 207 208 1.
FT REPEAT 209 210 2.
FT REPEAT 211 212 3.
FT REPEAT 211 212 4.
FT DOMAIN 261 305 OMPA-LIKE.
FT DISULFID 315 327 BY SIMILARITY.
SQ SEQUENCE 350 AA; 37575 MW; 6276C6F2F21065DA CRC64;

Query Match 15.4%; Score 53; DB 1; Length 350;
Best Local Similarity 100.0%; Pred. No. 2.7e-47;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 FTLKSDVLFNFKNATLKPEGOQALDQLYTQLSNMDPKDGSAAVVLGYTDRIGSE 265
Db 219 FTLKSDVLFNFKNATLKPEGOQALDQLYTQLSNMDPKDGSAAVVLGYTDRIGSE 271

RESULT 3
OMPA_CITFR
ID OMPA_CITFR STANDARD; PRT; 238 AA.
AC P24016;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Outer membrane protein A (Outer membrane protein II) (Fragment).
GN OMPA.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

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OC Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OS60;
RX MEDLINE-92065252; PubMed-1955870;
RA Lawrence J.G., Ochman H., Hartl D.L.;
RT "Molecular and evolutionary relationships among enteric bacteria.";
RL J. Gen. Microbiol. 137:1911-1921(1991).
CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
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CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
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CC -1- SUBUNIT: MONOMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
CC
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DR EMBL: M63354; AAA23095.1;
DR HSP; P02934; IQJP.
DR InterPro: IPR001145; Bac_OmpA.
DR Pfam: PF00691; OmpA; 1.
DR PRINTS: PR01021; OmpA_membrane; 1.
DR PRODOM: PD000930; Bac_OmpA; 1.
DR PROSITE: PS01068; OmpA; 1.
KW Outer membrane; Transmembrane; Phage recognition; Repeat; Porin.
FT SIGNAL 1 1
FT CHAIN 2 8
FT TRANSMEM <1 8 POTENTIAL.
FT TRANSMEM 12 27 POTENTIAL.
FT TRANSMEM 43 54 POTENTIAL.
FT TRANSMEM 60 76 POTENTIAL.
FT TRANSMEM 82 93 POTENTIAL.
FT DOMAIN 104 109 3 X 2 AA TANDEM REPEATS OF A-P.
FT REPEAT 104 105 1.
FT REPEAT 106 107 2.
FT REPEAT 108 109 3.
FT DOMAIN 138 202 OMPA-LIKE.
FT DISULFID 212 224 BY SIMILARITY.
FT NON_TER 238 238
SQ SEQUENCE 238 AA; 25664 MW; 66EA136D73A3F286 CRC64;

Query Match 12.5%; Score 43; DB 1; Length 238;
Best Local Similarity 100.0%; Pred. No. 5.2e-37;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 KISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 334
Db 195 KISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG 237

RESULT 4
OMPA_ECOLI
ID OMPA_ECOLI STANDARD; PRT; 346 AA.
AC P02934;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Outer membrane protein A precursor (Outer membrane protein II*).
GN OMPA OR TOLG OR TUT OR CON OR B0957 OR 21307 OR Ecs1041.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;

```

RA [1] SEQUENCE FROM N.A.
RP STRAIN-K12;
RX MEDLINE-81053729; PubMed-6253901;
RA Beck E., Bremer E.;
RT "Nucleotide sequence of the gene ompA coding the outer membrane
RL protein II of Escherichia coli K-12";
RN Nucleic Acids Res. 8:3011-3024(1980).
[2]
RA SEQUENCE FROM N.A.
RP STRAIN-K12;
RX MEDLINE-81170587; PubMed-6260951;
RA Movva N.R., Nakamura K., Inouye M.;
RT "Gene structure of the OmpA protein, a major surface protein of
RL Escherichia coli required for cell-cell interaction";
RN J. Mol. Biol. 143:317-328(1980).
[3]
RA SEQUENCE FROM N.A.
RP STRAIN-K12;
RX MEDLINE-97426617; PubMed-9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shaoy Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1233-1238(1997).
[4]
RA SEQUENCE FROM N.A.
RP STRAIN-K12;
RX MEDLINE-97061202; PubMed-8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikenoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampaio G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RL corresponding to the 12.7-28.0 min region on the linkage map";
RN DNA Res. 3:137-155(1996).
[5]
RA SEQUENCE FROM N.A.
RP STRAIN-O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE-21074935; PubMed-11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shaoy Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimailanta E.T., Potamocousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
[6]
RA SEQUENCE FROM N.A.
RP STRAIN-O157:H7 / RIMD 0509952;
RX MEDLINE-21156231; PubMed-11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RL O157:H7 and genomic comparison with a laboratory strain K-12";
RN DNA Res. 8:11-22(2001).
[7]
RA SEQUENCE OF 22-346.
RP STRAIN-K12;
RX MEDLINE-81054820; PubMed-7001461;
RA Chen R., Schmidmayr W., Kramer C., Chen-Schweissner U., Henning U.;
RT "Primary structure of major outer membrane protein II (ompA protein)
RL of Escherichia coli K-12";
RN Proc. Natl. Acad. Sci. U.S.A. 77:4592-4596(1980).
[8]
RA SEQUENCE OF 22-32.
RP STRAIN-K12 / W3110;
RA Pasquali C., Sanchez J.-C., Ravier F., Golaz O., Hughes G.J.,
RA Frutiger S., Paquet N., Wilkins M., Appel R.D., Baloch A.,
RA Hochstrasser D.F.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
[9]
RA SEQUENCE OF 22-34.
RP STRAIN-K12 / EMG2;
RX MEDLINE-97443975; PubMed-9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RL in the genome of Escherichia coli K-12";
RN Electrophoresis 18:1259-1313(1997).
[10]
RA SEQUENCE OF 22-26.
RP STRAIN-K12 / W3110;
RX MEDLINE-98291876; PubMed-9629924;
RA Molloy M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traini M.,
RA Sanchez J.-C., Hochstrasser D.F., Williams K.L., Gooley A.A.;
RT "Extraction of membrane proteins by differential solubilization for
RL separation using two-dimensional gel electrophoresis";
RN Electrophoresis 19:837-844(1998).
[11]
RA MUTANTS RESISTANT TO PHAGE ENTRY.
RP MEDLINE-84264337; PubMed-6086577;
RA Morona R., Klose M., Henning U.;
RT "Escherichia coli K-12 outer membrane protein (OmpA) as a
RL bacteriophage receptor: analysis of mutant genes expressing altered
RN proteins";
RX J. Bacteriol. 159:570-578(1984).
[12]
RA MUTANTS RESISTANT TO PHAGE ENTRY.
RP MEDLINE-86033606; PubMed-3902787;
RA Morona R., Kramer C., Henning U.;
RT "Bacteriophage receptor area of outer membrane protein OmpA of
RL Escherichia coli K-12";
RN J. Bacteriol. 164:539-543(1985).
[13]
RA PORIN ACTIVITY.
RP STRAIN-K12;
RX MEDLINE-92129334; PubMed-1370823;
RA Sugawara E., Nikaido H.;
RT "Pore-forming activity of OmpA protein of Escherichia coli";
RN J. Biol. Chem. 267:2507-2511(1992).
[14]
RA TOPOLOGY.
RP MEDLINE-94148615; PubMed-8106193;
RA Gromiha M.M., Ponnuswamy P.K.;
RT "Prediction of transmembrane beta-strands from hydrophobic
RL characteristics of proteins";
RN Int. J. Pept. Protein Res. 42:420-431(1993).
[15]
RA TOPOLOGY.
RP MEDLINE-99296577; PubMed-10368142;
RA Koebnik R.;
RT "Structural and functional roles of the surface-exposed loops of the
RL beta-barrel membrane protein OmpA from Escherichia coli";
RN J. Bacteriol. 181:3688-3694(1999).
[16]
RA X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 22-192.
RP MEDLINE-99023200; PubMed-9808047;
RA Pautsch A., Schulz G.E.;
RT "Structure of the outer membrane protein A transmembrane domain";
RN Nat. Struct. Biol. 5:1013-1017(1998).
[17]
RA X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
RP MEDLINE-20229895; PubMed-10764596;
RA Pautsch A., Schulz G.E.;
RT "High-resolution structure of the OmpA membrane domain";
RN J. Mol. Biol. 298:273-282(2000).
[18]
RA MASS SPECTROMETRY.
RP MEDLINE-2022957; PubMed-10757971;
RA le Coutre J., Whitelegge J.P., Gross A., Turk E., Wright E.M.,

RA Kaback H.R., Faull K.F.
RT "Proteomics on full-length membrane proteins using mass
RL spectrometry."
CC BIOCHEMISTRY 39:4237-4242(2000).
CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
CC SOLUTES.
CC -1- SUBUNIT: MONOMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -1- MASS SPECTROMETRY: MW=35177; METHOD=Electrospray; RANGE=22-346.
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
CC
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CC
CC EMBL: V00307; CAA23588.1; -
CC EMBL: AE000198; AAC74043.1; -
CC EMBL: D90733; BAA35715.1; -
CC EMBL: D90734; BAA35722.1; -
CC EMBL: AE005286; AAC55443.1; -
CC EMBL: AP002554; BAB34464.1; -
CC PIR: A03434; MMECA
CC PDB: 1BXW; 30-DEC-98.
CC PDB: 1QJP; 30-JUN-00.
CC SWISS-2DPAGE; P02934; COLI.
CC ECO2DBASE; F024.5; 6TH EDITION.
CC ECO2DBASE; F028.0; 6TH EDITION.
CC ECO2DBASE; F033.0; 6TH EDITION.
CC ECO2DBASE; F033.1; 6TH EDITION.
CC EcoGene; EG10669; ompA.
CC InterPro: IPR001145; Bac_OmpA.
CC InterPro: IPR000498; OmpA_tmemb.
CC Pfam; PF00691; OmpA; 1.
CC PRINTS; PR01021; OMPADOMAIN.

Query Match 9.6%; Score 33; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 87 KAQGVQLTKALGYPIITDDLDIYRLGGMVVRAD 119
DB 94 KAQGVQLTKALGYPIITDDLDIYRLGGMVVRAD 126
|||||

RESULT 5
OMPA_ESCFE STANDARD; PRT; 243 AA.
AC P24754;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Outer membrane protein A (Outer membrane protein II) (Fragment).
GN OMPA.
OS Escherichia hermannii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 33650, and ATCC 33652;
RX MEDLINE-92065252; PubMed-1955870;
RA Lawrence J.G., Ochman H., Hartl D.L.;
RT "Molecular and evolutionary relationships among enteric bacteria."
RL J. Gen. Microbiol. 137:1911-1921(1991).
CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE

CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
CC SOLUTES (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M63346; AAA24234.1; -
CC EMBL: M63347; AAA24238.1; -
CC HSP; P02934; IBXW.
CC InterPro: IPR001145; Bac_OmpA.
CC InterPro: IPR000498; OmpA_tmemb.
CC Pfam; PF00691; OmpA; 1.
CC ProDom; PD000930; Bac_OmpA; 1.
CC PROSITE; PS01068; OMPA; 1.
KW Outer membrane; Transmembrane; Phage recognition; Repeat; Porin.
FT NON_TER 1 1
FT TRANSMEM <1 8 POTENTIAL.
FT TRANSMEM 12 27 POTENTIAL.
FT TRANSMEM 47 58 POTENTIAL.
FT TRANSMEM 64 80 POTENTIAL.
FT TRANSMEM 86 97 POTENTIAL.
FT DOMAIN 107 114 4 X 2 AA TANDEM REPEATS OF A-P.
FT REPEAT 107 108 1.
FT REPEAT 109 110 2.
FT REPEAT 111 112 3.
FT REPEAT 113 114 4.
FT DOMAIN 163 207 OMPA-LIKE.
FT DISULFID 217 229 BY SIMILARITY.
FT NON_TER 243 243
SQ SEQUENCE 243 AA; 26202 MW; AA6CB6BA390D1E9D CRC64;
Query Match 8.4%; Score 29; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 210 TKHFTLKSDVLFNFNFKATLKPEGQALDQ 238
DB 118 TKHFTLKSDVLFNFNFKATLKPEGQALDQ 146
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RESULT 6
OMPA_ESCFE STANDARD; PRT; 243 AA.
AC P24747;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Outer membrane protein A (Outer membrane protein II) (Fragment).
GN OMPA.
OS Escherichia fergusonii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=564;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 35471, ATCC 35469, and ATCC 35472;
RX MEDLINE-92065252; PubMed-1955870;
RA Lawrence J.G., Ochman H., Hartl D.L.;
RT "Molecular and evolutionary relationships among enteric bacteria."
RL J. Gen. Microbiol. 137:1911-1921(1991).
CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A

```

CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
CC SOLUTES (BY SIMILARITY).
CC -|- SUBUNIT: MONOMER (PROBABLE).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -|- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAINS ATCC 35471
CC AND ATCC 35472.
CC -|- SIMILARITY: BELONGS TO THE OMPA FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M63352; AAA24236.1; -
CC EMBL: M63351; AAA24232.1; -
CC EMBL: M63353; AAA24240.1; -
CC HSSP: P02934; IQJP.
CC InterPro: IPR001145; Bac_OmpA.
CC InterPro: IPR000498; OmpA_tmem.
CC Pfam: PF00691; OmpA; 1.
CC Pfam: PF01389; OmpA_membrane; 1.
CC ProDom: PD000930; Bac_OmpA; 1.
CC ProSite: PS01068; OmpA; 1.
CC Outer membrane; Transmembrane; Phage recognition; Repeat; Porin.
KW NON_TER 1 1
FT TRANSMEM <1 8 POTENTIAL.
FT TRANSMEM 12 27 POTENTIAL.
FT TRANSMEM 48 59 POTENTIAL.
FT TRANSMEM 65 81 POTENTIAL.
FT TRANSMEM 87 98 POTENTIAL.
FT DOMAIN 107 114 4 X 2 AA TANDEM REPEATS OF A-P.
FT REPEAT 107 108 1.
FT REPEAT 109 110 2.
FT REPEAT 111 112 3.
FT REPEAT 113 114 4.
FT DOMAIN 163 207 OMPA-LIKE.
FT DISULFID 217 229 BY SIMILARITY.
FT VARIANT 39 39 E -> D (IN STRAIN ATCC 35469).
FT NON_TER 243 243
SQ SEQUENCE 243 AA; 26144 MW; B89F7FC29DA2E3AB CRC64;

Query Match 7.9%; Score 27; DB 1; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 LTAKLGYPIITDDLDIYTRLGGMVWRAD 119
Db 1 LTAKLGYPIITDDLDIYTRLGGMVWRAD 27
|||||
RESULT 7
ID OMPA_SHIDY STANDARD; PRT; 351 AA.
AC P02935;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Outer membrane protein A precursor (Outer membrane protein II).
GN OMPA.
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella.
OX NCBI_TaxID=622;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82221414; PubMed=6283478;
RA Braun G., Cole S.T.;
RT "The nucleotide sequence coding for major outer membrane protein OmpA
of Shigella dysenteriae."

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RL Nucleic Acids Res. 10:2367-2378(1982).
CC -|- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
CC SOLUTES (BY SIMILARITY).
CC -|- SUBUNIT: MONOMER (PROBABLE).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -|- SIMILARITY: BELONGS TO THE OMPA FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: V01344; CAA24638.1; -
CC PIR: A03435; MMEBAD.
CC HSSP: P02934; IQJP.
CC InterPro: IPR001145; Bac_OmpA.
CC InterPro: IPR000498; OmpA_tmem.
CC Pfam: PF00691; OmpA; 1.
CC Pfam: PF01389; OmpA_membrane; 1.
CC PRINTS: PR01021; OMPADOMAIN.
CC ProDom: PD000930; Bac_OmpA; 1.
CC ProSite: PS01068; OmpA; 1.
CC Outer membrane; Transmembrane; Phage recognition; Signal; Repeat;
KW Porin.
FT SIGNAL 1 21
FT CHAIN 22 351 OUTER MEMBRANE PROTEIN A.
FT TRANSMEM 27 40 POTENTIAL.
FT TRANSMEM 55 67 POTENTIAL.
FT TRANSMEM 70 85 POTENTIAL.
FT TRANSMEM 97 107 POTENTIAL.
FT TRANSMEM 111 126 POTENTIAL.
FT TRANSMEM 147 158 POTENTIAL.
FT TRANSMEM 164 180 POTENTIAL.
FT TRANSMEM 186 197 POTENTIAL.
FT DOMAIN 206 213 4 X 2 AA TANDEM REPEATS OF A-P.
FT REPEAT 206 207 1.
FT REPEAT 208 209 2.
FT REPEAT 210 211 3.
FT REPEAT 212 213 4.
FT DOMAIN 262 306 OMPA-LIKE.
FT DISULFID 316 328 BY SIMILARITY.
FT SEQUENCE 351 AA; 37741 MW; 1499AA5F5395B35B CRC64;

Query Match 7.0%; Score 24; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 4.8e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 TKHFTLKSDVLFNFNKATLKPEGQ 233
Db 217 TKHFTLKSDVLFNFNKATLKPEGQ 240
|||||
RESULT 8
ID OMPA_SALTY STANDARD; PRT; 350 AA.
AC P02936;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Outer membrane protein A precursor (Outer membrane protein 33k) (Outer
DE membrane major heat-modifiable protein).
GN OMPA OR STM1070.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]

```

SEQUENCE FROM N.A.
 RX MEDLINE=83287368; PubMed=6349993;
 RA Freidl R., Cole S.T.;
 RT "Cloning and molecular characterization of the ompA gene from
 RL Salmonella typhimurium";
 RN Eur. J. Biochem. 134:497-502(1983).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 LT2";
 RN Nature 413:852-856(2001).
 CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
 CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
 CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
 CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
 CC SOLUTES (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
 CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
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 CC EMBL; X02006; CAA26037.1; -
 CC EMBL; AE08746; AAL20003.1; -
 CC PIR; A03436; MMEBAT.
 CC HSP; P02934; IQJP.
 CC SyGene; SG10283; ompA.
 CC InterPro; IPR001145; Bac_OmpA.
 CC InterPro; IPR000498; OmpA_tmnm.
 CC Pfam; PF00691; OmpA; 1.
 CC Pfam; PF01389; OmpA_membrane; 1.
 CC ProDom; PD000930; Bac_OmpA; 1.
 CC PROSITE; PS01068; OmpA; 1.
 CC Outer membrane; Transmembrane; Phage recognition; Signal; Repeat;
 KW Porin; Complete proteome.
 FT SIGNAL 1 21
 FT CHAIN 22 350 OUTER MEMBRANE PROTEIN A.
 FT TRANSMEM 27 40 POTENTIAL.
 FT TRANSMEM 55 67 POTENTIAL.
 FT TRANSMEM 70 85 POTENTIAL.
 FT TRANSMEM 97 107 POTENTIAL.
 FT TRANSMEM 111 126 POTENTIAL.
 FT TRANSMEM 146 157 POTENTIAL.
 FT TRANSMEM 163 179 POTENTIAL.
 FT TRANSMEM 185 196 POTENTIAL.
 FT DOMAIN 205 212 4 X 2 AA TANDEM REPEATS OF A-P.
 FT REPEAT 205 206 1.
 FT REPEAT 207 208 2.
 FT REPEAT 209 210 3.
 FT REPEAT 211 212 4.
 FT DOMAIN 261 305 OMPA-LIKE.
 FT DISULFID 315 327 BY SIMILARITY.
 FT CONFLICT 114 114 V -> F (IN REF. 1).
 FT CONFLICT 247 247 S -> I (IN REF. 1).
 SQ SEQUENCE 350 AA; 37515 MW; B4AC52C8C5DF54FE CRC64;
 Query Match 6.4%; Score 22; DB 1; Length 350;
 Best Local Similarity 100.0%; Pred. No. 5.9e-15;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 KISARGMGESNPVTGNTCDNVK 313
 ||||||||||||||||||||
 Db 298 KISARGMGESNPVTGNTCDNVK 319
 ||||||||||||||||||||
 RESULT 9
 OMPA_ESCBL
 ID OMPA_ESCBL STANDARD; PRT; 241 AA.
 AC Q99124; Q03617;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Outer membrane protein A (Outer membrane protein II) (Fragment).
 GN OMPA.
 OS Escherichia blattae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=563;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33429, ATCC 29907, and ATCC 33430;
 RX MEDLINE=92065252; PubMed=1955870;
 RA Lawrence J.G., Ochman H., Hartl D.L.;
 RT "Molecular and evolutionary relationships among enteric bacteria";
 RL J. Gen. Microbiol. 137:1911-1921(1991).
 CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
 CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
 CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
 CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
 CC SOLUTES (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN ATCC 33429.
 CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M63343; AAA24235.1; -
 CC EMBL; M63344; AAA24239.1; -
 CC EMBL; M63345; AAA24242.1; -
 CC HSP; P02934; IQJP.
 CC InterPro; IPR001145; Bac_OmpA.
 CC InterPro; IPR000498; OmpA_tmnm.
 CC Pfam; PF00691; OmpA; 1.
 CC Pfam; PF01389; OmpA_membrane; 1.
 CC ProDom; PD000930; Bac_OmpA; 1.
 CC PROSITE; PS01068; OmpA; 1.
 CC Outer membrane; Transmembrane; Phage recognition; Repeat; Porin.
 FT NON_TER 1 1
 FT TRANSMEM <1 8 POTENTIAL.
 FT TRANSMEM 12 27 POTENTIAL.
 FT TRANSMEM 46 57 POTENTIAL.
 FT TRANSMEM 63 79 POTENTIAL.
 FT TRANSMEM 85 96 POTENTIAL.
 FT DOMAIN 105 112 4 X 2 AA TANDEM REPEATS OF A-P.
 FT REPEAT 105 106 1.
 FT REPEAT 107 108 2.
 FT REPEAT 109 110 3.
 FT REPEAT 111 112 4.
 FT DOMAIN 161 205 OMPA-LIKE.
 FT DISULFID 215 227 BY SIMILARITY.
 FT VARIANT 33 33 V -> G (IN STRAIN ATCC 29907).
 FT VARIANT 56 56 W -> M (IN STRAIN ATCC 33430).
 FT VARIANT 101 101 MISSING (IN STRAIN ATCC 33430).
 FT VARIANT 121 123 N -> S (IN STRAIN ATCC 29907 AND
 FT STRAIN ATCC 33430).
 FT VARIANT 220 220 K -> Q (IN STRAIN ATCC 29907 AND

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FT NON_TER 241 241 STRAIN ATCC 33430).
SQ SEQUENCE 241 AA; 25986 MW; 7C81CC0CCD5F1C40 CRC64;

Query Match
Best Local Similarity 5.8%; Score 20; DB 1; Length 241;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 315 RAALIDCLAPDRRVEIEVKG 334
DB 221 RAALIDCLAPDRRVEIEVKG 240

RESULT 10
OMPA_SERMA
ID OMPA_SERMA STANDARD; PRT; 359 AA.
AC P04845;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Outer membrane protein A precursor.
GN OMPA.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85035845; PubMed=6092858;
RA Braun G., Cole S.T.;
RT "DNA sequence analysis of the Serratia marcescens ompA gene:
RT implications for the organisation of an enterobacterial outer
RT membrane protein.";
RL Mol. Gen. Genet. 195;321-328(1984).
CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
CC SOLUTES (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
CC -----
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CC -----
CC EMBL; X00618; CAA25254.1;
CC PIR; S07298; S07298.
CC HSP; P02934; IQJP.
CC InterPro: IPR001145; Bac_OmpA.
CC InterPro: IPR000498; OmpA_tmem.
CC Pfam; PF00691; OmpA; 1.
CC PRINTS; PR01021; OMPA_DOMAIN.
CC ProDom; PD000930; Bac_OmpA; 1.
CC PROSITE; PS01068; OmpA; 1.
KW Outer membrane; Transmembrane; Phage recognition; Signal; Repeat;
KW Porin.
FT SIGNAL 1 21
FT CHAIN 22 359 OUTER MEMBRANE PROTEIN A.
FT TRANSMEM 27 40 POTENTIAL.
FT TRANSMEM 62 74 POTENTIAL.
FT TRANSMEM 77 92 POTENTIAL.
FT TRANSMEM 104 114 POTENTIAL.
FT TRANSMEM 118 133 POTENTIAL.
FT TRANSMEM 154 165 POTENTIAL.
FT TRANSMEM 171 187 POTENTIAL.
FT TRANSMEM 193 204 POTENTIAL.

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FT DOMAIN 210 219 5 X 2 AA TANDEM REPEATS OF A-P.
FT REPEAT 210 219 1.
FT REPEAT 212 213 3.
FT REPEAT 214 215 4.
FT REPEAT 216 217 5.
FT REPEAT 218 219 5.
FT DOMAIN 268 312 OMPA-LIKE.
FT DISULFID 322 336 BY SIMILARITY.
SQ SEQUENCE 359 AA; 38426 MW; 13992A037C19758B CRC64;

Query Match
Best Local Similarity 5.5%; Score 19; DB 1; Length 359;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 DLDLIYTRLGGMVWRADSK 121
DB 117 DLDLIYTRLGGMVWRADSK 135

RESULT 11
OMPA_SEROD
ID OMPA_SEROD STANDARD; PRT; 243 AA.
AC P24755;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Outer membrane protein A (Outer membrane protein II) (Fragment).
GN OMPA.
OS Serratia odorifera.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=618;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 3307;
RX MEDLINE=92065252; PubMed=1955870;
RA Lawrence J.G., Ochman H., Hartl D.L.;
RT "Molecular and evolutionary relationships among enteric bacteria.";
RT J. Gen. Microbiol. 137:1911-1921(1991).
CC -1- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
CC SOLUTES (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
CC -----
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CC -----
CC EMBL; M63357; AAA26561.1;
CC HSP; P02934; IQJP.
CC InterPro: IPR001145; Bac_OmpA.
CC InterPro: IPR000498; OmpA_tmem.
CC Pfam; PF00691; OmpA; 1.
CC Pfam; PF01389; OmpA; 1.
CC ProDom; PD000930; Bac_OmpA; 1.
CC PROSITE; PS01068; OmpA; FALSE_NEG.
KW Outer membrane; Transmembrane; Phage recognition; Repeat; Porin.
FT NON_TER 1 8
FT TRANSMEM <1 27 POTENTIAL.
FT TRANSMEM 12 27 POTENTIAL.
FT TRANSMEM 48 59 POTENTIAL.
FT TRANSMEM 65 81 POTENTIAL.
FT TRANSMEM 87 98 POTENTIAL.
FT DOMAIN 104 113 5 X 2 AA TANDEM REPEATS OF A-P.
FT REPEAT 104 105 1.

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FT REPEAT 106 107 2.
FT REPEAT 108 109 3.
FT REPEAT 110 111 4.
FT REPEAT 112 113 5.
FT DISULFID 215 229 BY SIMILARITY.
FT NON_TER 243 243
SQ SEQUENCE 243 AA; 25972 MW; 687CC9C10DDEC64C CRC64;

Query Match
Best Local Similarity 4.9%; Score 17; DB 1; Length 243;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 LKPEGQALDQLYTOLS 244
DB 135 LKPEGQALDQLYTOLS 151

RESULT 12
ID OMPA_BUCAI STANDARD; PRT; 349 AA.
AC P57414;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE OmpA-like protein precursor.
GN OMPA OR BU332
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: ACTS AS A PORE WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL SOLUTES (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
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CC -----
DR EMBL; AF001119; BAB13037.1; -.
DR HSSP; P02934; IQJP.
DR InterPro; IPR001145; Bac_OmpA.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRODOM; PD000930; Bac_OmpA; 1.
DR PROSITE; PS01068; OMPA; FALSE_NEG.
KW Transmembrane; Porin; Signal; Complete proteome.
FT SIGNAL 1 22
FT CHAIN 23 349 POTENTIAL.
FT TRANSMEM 27 40 POTENTIAL.
FT TRANSMEM 63 75 POTENTIAL.
FT TRANSMEM 78 93 POTENTIAL.
FT TRANSMEM 106 116 POTENTIAL.
FT TRANSMEM 120 135 POTENTIAL.
FT TRANSMEM 154 165 POTENTIAL.
FT TRANSMEM 171 187 POTENTIAL.
FT TRANSMEM 193 204 POTENTIAL.
FT DOMAIN 207 218 HINGE LIKE.
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FT DOMAIN 267 311 OMPA-LIKE.
FT DISULFID 321 333 BY SIMILARITY.
SQ SEQUENCE 349 AA; 39303 MW; CC14AB1BD590CF58 CRC64;

Query Match
Best Local Similarity 3.5%; Score 12; DB 1; Length 349;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 CLAPDRRVEIEV 332
DB 333 CLAPDRRVEIEV 344

RESULT 13
ID OM52_HAEIN STANDARD; PRT; 353 AA.
AC P38368;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Outer membrane protein P5 precursor (OMP P5).
GN OMPA OR OMPp5.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-34.
RC STRAIN=1613 / Serotype B;
RX MEDLINE=93366472; PubMed=8359929;
RA Munson R.S. Jr., Grass S., West R.;
RT "Molecular cloning and sequence of the gene for outer membrane protein P5 of Haemophilus influenzae.";
RL Infect. Immun. 61:4017-4020(1993).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
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CC -----
DR EMBL; L20309; AAA03346.1; -.
DR HSSP; P02934; IQJP.
DR InterPro; IPR001145; Bac_OmpA.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRODOM; PD000930; Bac_OmpA; 1.
DR PROSITE; PS01068; OMPA; 1.
KW Outer membrane; Transmembrane; Porin; Signal.
FT SIGNAL 1 21
FT CHAIN 22 353 OUTER MEMBRANE PROTEIN P5.
FT DISULFID 326 338 BY SIMILARITY.
FT DOMAIN 272 316 OMPA-LIKE.
SQ SEQUENCE 353 AA; 37594 MW; E58A659E786D0D0F7 CRC64;

Query Match
Best Local Similarity 2.9%; Score 10; DB 1; Length 353;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 CLAPDRRVEI 330
DB 338 CLAPDRRVEI 347

RESULT 14
ID OM53_HAEIN STANDARD; PRT; 359 AA.
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AC P45996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Outer membrane protein P5 precursor (OMP P5) (Fimbrin).
GN OMPA OR OMPPS.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus
OC NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=NTHI 1128;
RX MEDLINE=94222575; PubMed=7909539;
RA Sirakova T., Kollatukudy P.E., Murwin D., Billy J., Leake E.,
RL "Role of fimbriae expressed by nontypeable Haemophilus influenzae in
RT pathogenesis of and protection against otitis media and relatedness
FT of the fimbriae subunit to outer membrane protein A.";
RL Infect. Immun. 62:2002-2020(1994).
CC -1- FUNCTION: ACTS AS A FIMBRIAE SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -1- SIMILARITY: BELONGS TO THE OMPA FAMILY.
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CC -----
EMBL: L08448; AAA24959.1;
DR HSP; P02934; IBXW.
DR InterPro: IPR001145; Bac_OmpA.
DR InterPro: IPR000498; OmpA_tmern.
DR Pfam: PF00691; OmpA; 1.
DR Pfam: PF01389; OmpA_membrane; 1.
DR PRINTS: PR01021; OMPADOMAIN.
DR PRODOM: PD000830; Bac_OmpA; 1.
DR PROSITE: PS01068; OMPA; FALSE_NEG.
KW Outer membrane; Transmembrane; Porin; Signal; Fimbria.
FT SIGNAL 1 21
FT CHAIN 22 359 OUTER MEMBRANE PROTEIN P5.
FT DISULFID 332 344 BY SIMILARITY.
FT DOMAIN 278 322 OMPA-LIKE.
SQ SEQUENCE 359 AA; 38340 MW; 576B1C59B4818C37 CRC64;

Query Match 2.9%; Score 10; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 CLAPDRRVEI 330
DB 344 CLAPDRRVEI 353

RESULT 15
MLE1_MUGCA
ID MLE1_MUGCA STANDARD; PRT; 186 AA.
AC P82159;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin light chain 1, skeletal muscle isoform (Al catalytic) (Alkali)
DE (LC-1) (LC1).
OS Mugil capito (Grey mullet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Mugilomorpha; Mugilidae;
OC Liza.
OX NCBI_TaxID=30804;
RN [1]

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RP SEQUENCE.
RC TISSUE=Fast muscle;
RX MEDLINE=92042685; PubMed=1939601;
RA dalla Libera L., Carpenne E., Theibert J., Collins J.H.;
RT "Fish myosin alkali light chains originate from two different genes.";
RL J. Muscle Res. Cell Motil. 12:366-371(1991).
CC -1- SUBUNIT: MYOSIN IS A HEXAMER OF 2 HEAVY CHAINS & 4 LIGHT CHAINS.
CC -1- MISCELLANEOUS: IN FISH, MYOSIN MLC1 AND MLC3 APPEAR TO BE PRODUCED
CC BY TWO DIFFERENT GENES UNLIKE IN BIRDS AND MAMMALS, WHERE THEY ARE
CC PRODUCED FROM A SINGLE GENE BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BUT THIS
CC PROTEIN DOES NOT BIND CALCIUM.
DR HSP; P02607; IBRI.
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; efhand; 2.
DR PRODOM: PD000012; EF-hand; 2.
KW Myosin; Muscle protein.
FT MOD_RES 1 1
SQ SEQUENCE 186 AA; 20067 MW; 57306F13CDE9E639 CRC64;

Query Match 2.6%; Score 9; DB 1; Length 186;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 APAPAPAPE 207
DB 12 APAPAPAPE 20

Search completed: April 15, 2003, 08:55:36
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: April 15, 2003, 08:51:59 ; Search time 34 Seconds
(without alignments)
2084.712 Million cell updates/sec

Title: US-09-831-061-2

Perfect score: 344

Sequence: 1 MKAIFVLNAPKDNVTWAGG.....DRRVEIEVKGKVVQTQAG 344

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 5

Total number of hits satisfying chosen parameters: 39383

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

SPTREMBL_21.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	15.4	238	Q91114	Q91114 escherichia
2	36	10.5	238	Q91123	Q91123 enterobacte
3	33	9.6	148	Q93Q11	Q93Q11 erwinia per
4	33	9.6	246	Q91618	Q91618 shigella fl
5	29	8.4	244	Q47880	Q47880 escherichia
6	29	8.4	244	Q91115	Q91115 escherichia
7	28	8.1	148	Q93QR2	Q93QR2 erwinia psi
8	28	8.1	148	Q93QR1	Q93QR1 erwinia psi
9	28	8.1	148	Q93QR0	Q93QR0 erwinia psi
10	28	8.1	148	Q93QR4	Q93QR4 erwinia psi
11	28	8.1	149	Q93QR3	Q93QR3 erwinia psi
12	28	8.1	149	Q93QR2	Q93QR2 erwinia rha
13	26	7.6	149	Q93QR2	Q93QR2 erwinia rha
14	22	6.4	147	Q93QR5	Q93QR5 erwinia mal
15	22	6.4	149	Q93QR5	Q93QR5 erwinia mal
16	22	6.4	149	Q93QR4	Q93QR4 erwinia mal

17	22	6.4	346	2	Q916J0	Q916J0 escherichia
18	22	6.4	350	16	Q827S0	Q827S0 salmonella
19	22	6.4	353	16	Q82G77	Q82G77 verginia pe
20	21	6.1	147	2	Q93Q88	Q93Q88 erwinia chr
21	21	6.1	149	2	Q93Q85	Q93Q85 erwinia mal
22	21	6.1	149	2	Q93Q84	Q93Q84 erwinia tra
23	21	6.1	149	2	Q93Q80	Q93Q80 erwinia tra
24	20	5.8	249	2	Q93Q87	Q93Q87 brenneria r
25	20	5.8	249	2	Q91619	Q91619 salmonella
26	19	5.5	147	2	Q93Q83	Q93Q83 erwinia tra
27	19	5.5	147	2	Q93Q82	Q93Q82 erwinia tra
28	19	5.5	149	2	Q93Q83	Q93Q83 erwinia amy
29	19	5.5	149	2	Q93Q82	Q93Q82 erwinia amy
30	19	5.5	149	2	Q93Q81	Q93Q81 erwinia amy
31	19	5.5	149	2	Q93Q80	Q93Q80 erwinia amy
32	19	5.5	149	2	Q93Q89	Q93Q89 erwinia amy
33	19	5.5	149	2	Q93Q88	Q93Q88 erwinia amy
34	19	5.5	149	2	Q93Q87	Q93Q87 erwinia amy
35	19	5.5	149	2	Q93Q86	Q93Q86 erwinia amy
36	19	5.5	149	2	Q93Q85	Q93Q85 erwinia amy
37	19	5.5	149	2	Q93Q84	Q93Q84 erwinia amy
38	19	5.5	149	2	Q93Q83	Q93Q83 erwinia amy
39	19	5.5	149	2	Q93Q82	Q93Q82 erwinia amy
40	19	5.5	149	2	Q93Q81	Q93Q81 erwinia amy
41	19	5.5	149	2	Q93Q80	Q93Q80 erwinia amy
42	19	5.5	149	2	Q93Q77	Q93Q77 erwinia amy
43	19	5.5	149	2	Q93Q75	Q93Q75 erwinia amy
44	19	5.5	149	2	Q93Q74	Q93Q74 erwinia amy
45	19	5.5	149	2	Q93Q71	Q93Q71 erwinia amy
46	19	5.5	149	2	Q93Q70	Q93Q70 erwinia amy
47	19	5.5	149	2	Q93Q68	Q93Q68 erwinia amy
48	19	5.5	149	2	Q93Q66	Q93Q66 erwinia amy
49	19	5.5	149	2	Q93Q65	Q93Q65 erwinia amy
50	19	5.5	149	2	Q93Q64	Q93Q64 erwinia amy
51	19	5.5	149	2	Q93Q63	Q93Q63 erwinia amy
52	19	5.5	149	2	Q93Q62	Q93Q62 erwinia amy
53	19	5.5	149	2	Q93Q57	Q93Q57 erwinia amy
54	19	5.5	149	2	Q93Q55	Q93Q55 erwinia amy
55	19	5.5	149	2	Q93Q52	Q93Q52 erwinia amy
56	19	5.5	149	2	Q93Q51	Q93Q51 erwinia amy
57	19	5.5	149	2	Q93Q48	Q93Q48 erwinia amy
58	19	5.5	149	2	Q93Q47	Q93Q47 erwinia amy
59	19	5.5	149	2	Q93Q46	Q93Q46 erwinia amy
60	18	5.2	145	2	Q93Q45	Q93Q45 erwinia car
61	18	5.2	146	2	Q93Q48	Q93Q48 erwinia tra
62	18	5.2	147	2	Q93Q49	Q93Q49 brenneria r
63	18	5.2	149	2	Q93Q59	Q93Q59 erwinia amy
64	18	5.2	149	2	Q93Q58	Q93Q58 erwinia amy
65	18	5.2	149	2	Q93Q57	Q93Q57 erwinia amy
66	18	5.2	149	2	Q93Q56	Q93Q56 erwinia amy
67	18	5.2	149	2	Q93Q55	Q93Q55 erwinia amy
68	18	5.2	149	2	Q93Q54	Q93Q54 erwinia tra
69	17	4.9	149	2	Q93Q54	Q93Q54 erwinia tra
70	17	4.9	367	2	Q93Q59	Q93Q59 erwinia car
71	16	4.7	147	2	Q93Q49	Q93Q49 brenneria r
72	15	4.4	145	2	Q93Q47	Q93Q47 brenneria a
73	15	4.4	145	2	Q93Q40	Q93Q40 brenneria n
74	15	4.4	145	2	Q93Q39	Q93Q39 brenneria n
75	15	4.4	145	2	Q93Q38	Q93Q38 brenneria n
76	15	4.4	145	2	Q93Q37	Q93Q37 brenneria n
77	15	4.4	145	2	Q93Q36	Q93Q36 brenneria n
78	15	4.4	147	2	Q93Q35	Q93Q35 brenneria r
79	14	4.1	145	2	Q93Q33	Q93Q33 erwinia car
80	14	4.1	146	2	Q93Q34	Q93Q34 erwinia l
81	14	4.1	146	2	Q93Q33	Q93Q33 brenneria l
82	14	4.1	149	2	Q93Q31	Q93Q31 erwinia amy
83	14	4.1	149	2	Q93Q30	Q93Q30 erwinia amy
84	14	4.1	149	2	Q93Q29	Q93Q29 erwinia amy
85	14	4.1	149	2	Q93Q27	Q93Q27 erwinia amy
86	14	4.1	149	2	Q93Q26	Q93Q26 erwinia amy
87	14	4.1	149	2	Q93Q25	Q93Q25 erwinia amy
88	14	4.1	149	2	Q93Q24	Q93Q24 erwinia amy
89	14	4.1	149	2	Q93Q23	Q93Q23 erwinia amy

90	14	4.1	149	2	Q93056	Q93q56 erwinia amy	163	8	2.3	92	10	Q24350
91	14	4.1	149	2	Q93054	Q93q54 erwinia amy	164	8	2.3	94	16	Q8X6U0
92	14	4.1	149	2	Q93053	Q93q53 erwinia amy	165	8	2.3	97	10	Q8S017
93	14	4.1	149	2	Q93050	Q93q50 erwinia amy	166	8	2.3	129	2	Q57111
94	14	4.1	149	2	Q930R9	Q93qr9 erwinia amy	167	8	2.3	131	10	Q94A23
95	14	4.1	149	2	Q930R5	Q93qr5 erwinia amy	168	8	2.3	131	10	Q92T19
96	13	3.8	147	2	Q930N5	Q93qn5 brenneria s	169	8	2.3	134	2	Q54030
97	13	3.8	147	2	Q9A073	Q9aq73 erwinia amy	170	8	2.3	140	10	Q8RZM6
98	12	3.5	150	2	Q930N9	Q93qn9 pectobacter	171	8	2.3	142	2	Q9L5A0
99	11	3.2	147	2	Q930N6	Q93qn6 brenneria s	172	8	2.3	145	5	Q45192
100	11	3.2	147	2	Q930N4	Q93qn4 brenneria s	173	8	2.3	147	2	Q69087
101	11	3.2	147	2	Q930N3	Q93qn3 brenneria s	174	8	2.3	163	16	Q9A6B3
102	11	3.2	147	2	Q930N2	Q93qn2 brenneria s	175	8	2.3	164	13	Q90W45
103	11	3.2	147	2	Q930N1	Q93qn1 brenneria s	176	8	2.3	165	2	Q54279
104	10	2.9	106	2	Q9R659	Q9r659 proteus mir	177	8	2.3	166	5	Q9NFX6
105	10	2.9	236	5	Q9VDH1	Q9vdx1 drosophila	178	8	2.3	168	5	Q62008
106	10	2.9	339	2	Q44298	Q44298 aeromonas s	179	8	2.3	170	5	Q9VX77
107	10	2.9	341	2	Q8RJ58	Q8rj58 haemophilus	180	8	2.3	172	13	Q9IB35
108	10	2.9	344	2	Q8RMW2	Q8rmw2 haemophilus	181	8	2.3	181	10	Q9ZRE9
109	10	2.9	344	2	Q8RMW1	Q8rmw1 haemophilus	182	8	2.3	182	16	Q9CBW9
110	10	2.9	344	2	Q8RMW0	Q8rmw0 haemophilus	183	8	2.3	182	16	Q8XXW2
111	10	2.9	344	2	Q8RML9	Q8rml9 haemophilus	184	8	2.3	185	16	P90995
112	10	2.9	344	2	Q8RML8	Q8rml8 haemophilus	185	8	2.3	190	5	P90995
113	10	2.9	344	2	Q8RJD0	Q8rjd0 haemophilus	186	8	2.3	192	13	Q90895
114	10	2.9	346	2	Q9S5J9	Q9s5j9 actinobacil	187	8	2.3	192	4	Q03399
115	10	2.9	346	2	Q51841	Q51841 actinobacil	188	8	2.3	202	5	Q9VST6
116	10	2.9	378	2	Q9R028	Q9rq28 pasteurella	189	8	2.3	202	10	Q9AY46
117	9	2.6	146	2	Q93002	Q93qq2 brenneria l	190	8	2.3	214	2	Q93M22
118	9	2.6	146	2	Q93001	Q93qq1 brenneria q	191	8	2.3	216	16	Q9AAT5
119	9	2.6	146	2	Q930Q0	Q93qq0 brenneria q	192	8	2.3	221	16	Q8XY00
120	9	2.6	146	2	Q930P9	Q93qp9 brenneria q	193	8	2.3	225	2	Q9L591
121	9	2.6	146	2	Q930P8	Q93qp8 brenneria q	194	8	2.3	226	10	Q948H7
122	9	2.6	146	2	Q930P7	Q93qp7 brenneria q	195	8	2.3	227	16	Q95XQ6
123	9	2.6	148	2	Q930Q8	Q93qq8 brenneria r	196	8	2.3	227	5	O06556
124	9	2.6	187	16	P74534	P74534 synchocyst	197	8	2.3	230	16	Q8VK55
125	9	2.6	191	13	Q9IB30	Q9ib30 cypselurus	198	8	2.3	235	16	Q9IL37
126	9	2.6	192	13	Q9IB27	Q9ib27 trachurus t	199	8	2.3	240	12	Q9RSN5
127	9	2.6	193	13	Q9IB33	Q9ib33 pennahia ar	200	8	2.3	241	3	Q9P3A6
128	9	2.6	193	13	Q90331	Q90331 cyprinus ca	201	8	2.3	249	16	Q9L127
129	9	2.6	193	13	Q90332	Q90332 cyprinus ca	202	8	2.3	254	10	Q8VZA7
130	9	2.6	194	13	Q90W52	Q90w52 catanx deli	203	8	2.3	254	10	Q8S781
131	9	2.6	194	13	Q90W44	Q90w44 decapteris	204	8	2.3	260	11	O35455
132	9	2.6	197	13	Q90W46	Q90w46 decapteris	205	8	2.3	262	10	Q8W2Q2
133	9	2.6	198	13	Q9IB39	Q9ib39 thunnus thy	206	8	2.3	269	10	Q8S1F2
134	9	2.6	198	13	Q9IB36	Q9ib36 katsuwonus	207	8	2.3	283	4	Q9UKC7
135	9	2.6	198	13	Q90W41	Q90w41 scomber jap	208	8	2.3	283	4	Q9Y417
136	9	2.6	203	13	O12966	O12966 fugu rubrip	209	8	2.3	285	5	Q8SXU6
137	9	2.6	215	10	Q43719	Q43719 lycopersico	210	8	2.3	285	10	Q9AHY1
138	9	2.6	249	2	Q9L575	Q9l575 streptococc	211	8	2.3	288	16	Q9EMH8
139	9	2.6	310	5	Q9W496	Q9w496 drosophila	212	8	2.3	289	10	Q39563
140	9	2.6	326	2	Q9X4S0	Q9x4s0 pseudomonas	213	8	2.3	304	11	Q9D990
141	9	2.6	330	2	Q44299	Q44299 aeromonas s	214	8	2.3	308	10	Q8SB66
142	9	2.6	344	2	Q9LA97	Q9la97 aeromonas h	215	8	2.3	311	4	Q96RX7
143	9	2.6	361	10	Q9ZTY0	Q9zty0 emiliania h	216	8	2.3	319	2	Q9FIV0
144	9	2.6	403	2	P96773	P96773 haemophilus	217	8	2.3	321	2	Q93HK0
145	9	2.6	407	2	P96774	P96774 haemophilus	218	8	2.3	325	2	Q925X6
146	9	2.6	424	10	Q9FM65	Q9fm65 arabidopsis	219	8	2.3	325	10	Q8SB65
147	9	2.6	443	5	O76153	O76153 periplaneta	220	8	2.3	326	5	Q9NFX5
148	9	2.6	537	2	Q46977	Q46977 escherichia	221	8	2.3	326	5	O62010
149	9	2.6	537	16	Q989A5	Q989a5 rhizobium l	222	8	2.3	327	10	Q94GU0
150	9	2.6	581	5	Q20517	Q20517 caenorhabdi	223	8	2.3	332	5	Q9NFX7
151	9	2.6	594	4	O14772	O14772 homo sapien	224	8	2.3	332	5	O62009
152	9	2.6	706	5	Q9VVR5	Q9vyr5 drosophila	225	8	2.3	332	12	Q91GY8
153	9	2.6	883	2	Q9RF11	Q9rf11 myxococcus	226	8	2.3	334	12	Q91GY9
154	9	2.6	1013	5	Q9VVT7	Q9vvt7 drosophila	227	8	2.3	340	12	Q91GZ0
155	9	2.6	1061	16	Q8X8J5	Q8x8j5 escherichia	228	8	2.3	340	12	Q91GZ0
156	9	2.6	1453	4	Q9Y6T1	Q9y6t1 homo sapien	229	8	2.3	340	12	Q910T9
157	9	2.6	1606	11	Q924A2	Q924a2 mus musculu	230	8	2.3	344	11	O89037
158	9	2.6	1608	4	Q96RK0	Q96rk0 homo sapien	231	8	2.3	346	4	Q9NSQ9
159	9	2.6	1785	5	Q25685	Q25685 plasmodium	232	8	2.3	348	2	Q8VPL3
160	9	2.6	2163	5	Q9NFB6	Q9nfb6 plasmodium	233	8	2.3	353	16	Q9CMN1
161	8	2.3	15	2	Q9R564	Q9r564 escherichia	234	8	2.3	354	3	Q9VMZ5
162	8	2.3	90	5	Q9VW28	Q9vW28 drosophila	235	8	2.3	356	11	Q99L93

236	8	2.3	359	10	Q8RYA9	Q8rx9 zea mays (m	309	8	2.3	1046	4	Q9P2X1	Q9p2x1 homo sapien
237	8	2.3	360	2	Q86254	Q86254 haemophilus	310	8	2.3	1056	10	Q9FW41	Q9fw41 oryza sativ
238	8	2.3	361	12	Q9NMR9	Q9ymr9 lymantria d	311	8	2.3	1088	4	Q9NRM7	Q9nmr7 homo sapien
239	8	2.3	367	10	Q9LWE1	Q9lwe1 oryza sativ	312	8	2.3	1097	5	Q9O2T9	Q9o2t9 caenorhabdi
240	8	2.3	368	3	Q9P837	Q9p837 candida alb	313	8	2.3	1098	11	Q9WTN8	Q9wtm8 rattus norv
241	8	2.3	370	10	Q8S9W0	Q8s9w0 oryza sativ	314	8	2.3	1151	13	Q57580	Q57580 gallus gall
242	8	2.3	378	10	Q9SF49	Q9sf49 arabidopsis	315	8	2.3	1154	11	Q921R2	Q921r2 mus musculu
243	8	2.3	379	10	Q03991	Q03991 daucus caro	316	8	2.3	1360	3	Q9P422	Q9p422 neurospora
244	8	2.3	381	4	Q96Q15	Q96q15 homo sapien	317	8	2.3	1461	5	Q8T9F6	Q8t9f6 drosophila
245	8	2.3	382	5	Q9V105	Q9v1u5 drosophila	318	8	2.3	1474	5	Q8T4M0	Q8t4m0 drosophila
246	8	2.3	384	2	Q9LAY6	Q9lay6 streptococc	319	8	2.3	1500	5	Q8V1Q8	Q8vlq8 drosophila
247	8	2.3	385	2	Q9LAZ1	Q9laz1 streptococc	320	8	2.3	1503	5	Q8T4L8	Q8t4l8 drosophila
248	8	2.3	392	2	Q9LAY2	Q9lay2 streptococc	321	8	2.3	1509	5	Q9SP10	Q9sp10 drosophila
249	8	2.3	399	16	Q8XAP7	Q8xap7 escherichia	322	8	2.3	1513	5	Q17970	Q17970 caenorhabdi
250	8	2.3	406	2	Q9LAZ0	Q9laz0 streptococc	323	8	2.3	1553	5	Q9STR0	Q9str0 drosophila
251	8	2.3	408	2	Q9LAY0	Q9lay0 streptococc	324	8	2.3	1584	5	Q9J791	Q9jp78 bordetella
252	8	2.3	417	16	Q9FC63	Q9fc63 streptococc	325	8	2.3	1676	3	Q8TG36	Q8tg36 plasmodium
253	8	2.3	426	2	Q9LAY5	Q9lay5 streptococc	326	8	2.3	1678	11	Q924C5	Q924c5 mus musculu
254	8	2.3	437	2	Q9LAY4	Q9lay4 streptococc	327	8	2.3	1698	5	Q9V5J8	Q9v5j8 drosophila
255	8	2.3	438	16	Q9A2W5	Q9a2w5 caulobacter	328	8	2.3	1785	10	Q8S789	Q8s789 oryza sativ
256	8	2.3	439	10	Q9PWF7	Q9pwf7 oryza sativ	329	8	2.3	2110	5	Q9VRA6	Q9vra6 drosophila
257	8	2.3	442	10	Q9M4C5	Q9m4c5 avena fatua	330	8	2.3	2197	5	Q9G296	Q9g296 plasmodium
258	8	2.3	449	5	Q20198	Q20198 caenorhabdi	331	8	2.3	2634	2	Q9JP78	Q9jp78 bordetella
259	8	2.3	461	3	Q8X053	Q8x053 neurospora	332	8	2.3	3634	2	Q9J791	Q9jp78 bordetella
260	8	2.3	468	6	Q8BE23	Q8be23 macaca fasc	333	8	2.3	3689	16	Q8XS40	Q8xs40 raietonia s
261	8	2.3	468	10	Q8S5P0	Q8s5p0 oryza sativ	334	8	2.3	45	9	Q9NW6	Q9nw6 streptomyc
262	8	2.3	492	11	Q35392	Q35392 mus musculu	335	7	2.0	63	2	Q9F212	Q9f212 roseteles
263	8	2.3	493	3	Q9UVD1	Q9uvd1 pneumocysti	336	7	2.0	70	10	Q8S0T1	Q8s0t1 oryza sativ
264	8	2.3	500	16	Q9RT74	Q9rt74 deinozococcus	337	7	2.0	83	5	Q9W8V6	Q9w8v6 drosophila
265	8	2.3	508	2	Q9P8A6	Q9p8a6 treponema p	338	7	2.0	94	9	Q8W6Y8	Q8w6y8 cyanohege
266	8	2.3	533	4	Q9H5W9	Q9h5w9 homo sapien	339	7	2.0	102	12	Q9PXP5	Q9pxp5 hepatitis c
267	8	2.3	542	12	Q91CH9	Q91ch9 macropodid	340	7	2.0	102	12	Q9PXP4	Q9pxp4 hepatitis c
268	8	2.3	552	10	Q96343	Q96343 brassica na	341	7	2.0	108	17	Q9Y9N3	Q9y9n3 aeropyrum p
269	8	2.3	554	16	Q8X205	Q8x205 raietonia s	342	7	2.0	113	10	Q945Q3	Q945q3 arabidopsis
270	8	2.3	562	5	Q8T0S2	Q8t0s2 drosophila	343	7	2.0	113	17	Q97222	Q97222 sulfolobus
271	8	2.3	569	10	Q8W204	Q8w2q4 oryza sativ	344	7	2.0	118	16	Q8X220	Q8x220 raietonia s
272	8	2.3	581	5	Q9W0N9	Q9w0n9 drosophila	345	7	2.0	120	16	Q92B40	Q92b40 listeria in
273	8	2.3	582	16	Q9AAQ8	Q9aaq8 caulobacter	346	7	2.0	121	6	Q9BDC2	Q9bdg2 bos taurus
274	8	2.3	584	16	Q9AAZ3	Q9aaz3 caulobacter	347	7	2.0	127	5	Q9SRA0	Q9sra0 drosophila
275	8	2.3	590	16	Q9S2Q5	Q9s2q5 streptomyc	348	7	2.0	129	10	Q40615	Q40615 oryza rufip
276	8	2.3	596	16	Q9RSC6	Q9rsc6 deinozococcus	349	7	2.0	132	10	Q9SE04	Q9se04 oryza sativ
277	8	2.3	600	16	Q9HY28	Q9hy18 pseudomonas	350	7	2.0	139	10	Q9ZT17	Q9zt17 arabidopsis
278	8	2.3	605	16	Q9L1P6	Q9l1f6 streptomyc	351	7	2.0	139	10	Q8R2R5	Q8r2r5 oryza sativ
279	8	2.3	612	2	Q9Z614	Q9z614 streptomyc	352	7	2.0	143	4	Q9H4U5	Q9h4u5 homo sapien
280	8	2.3	642	10	Q23831	Q23831 arabidopsis	353	7	2.0	144	17	Q8U303	Q8u303 pyrococcus
281	8	2.3	643	10	Q9SSV0	Q9ssv0 arabidopsis	354	7	2.0	145	2	Q9ZAA7	Q9zaa7 acidaminoco
282	8	2.3	646	10	Q9SXH0	Q9sxh0 arabidopsis	355	7	2.0	147	2	Q07907	Q07907 rhodobacter
283	8	2.3	654	10	Q9M5W9	Q9m5w9 arabidopsis	356	7	2.0	155	12	Q8QNK4	Q8qnk4 ectocarpus
284	8	2.3	667	2	Q9KK28	Q9kk28 streptococc	357	7	2.0	156	16	Q8XSU0	Q8xsu0 raietonia s
285	8	2.3	667	11	Q9R1D9	Q9rid9 mus musculu	358	7	2.0	160	4	Q8TCG9	Q8tcg9 homo sapien
286	8	2.3	676	16	Q9XAR9	Q9xar9 streptomyc	359	7	2.0	163	13	Q90W43	Q90w43 decapteris
287	8	2.3	689	5	Q9GRF0	Q9grf0 caenorhabdi	360	7	2.0	166	5	Q9S268	Q9s268 osteria
288	8	2.3	693	16	Q83619	Q83619 treponema p	361	7	2.0	171	10	Q9C684	Q9c684 arabidopsis
289	8	2.3	719	2	P72539	P72539 streptomyc	362	7	2.0	171	13	Q9IB38	Q9ib38 thunnus thy
290	8	2.3	737	11	Q9WVF3	Q9wvf3 mus musculu	363	7	2.0	176	11	Q9D367	Q9d367 mus musculu
291	8	2.3	739	2	Q9R074	Q9rqt4 streptococc	364	7	2.0	180	10	Q9SHY3	Q9shy3 arabidopsis
292	8	2.3	744	3	Q9C2N3	Q9czn3 neurospora	365	7	2.0	181	5	Q8SWS3	Q8sws3 drosophila
293	8	2.3	747	5	Q9XU12	Q9xul2 caenorhabdi	366	7	2.0	187	2	Q9F814	Q9fb14 streptomyc
294	8	2.3	748	12	Q65820	Q65820 bovine heip	367	7	2.0	187	11	Q9ESU4	Q9esu4 mus musculu
295	8	2.3	753	5	Q93107	Q93107 acanthamoeb	368	7	2.0	188	11	Q9D7T0	Q9d7t0 mus musculu
296	8	2.3	784	16	Q9RKL5	Q9rk15 streptomyc	369	7	2.0	189	5	Q8S2D3	Q8szd3 drosophila
297	8	2.3	796	5	Q9VZB8	Q9vze8 drosophila	370	7	2.0	190	13	Q91792	Q91792 xenopus lae
298	8	2.3	806	11	Q9WVF4	Q9wvf4 mus musculu	371	7	2.0	193	2	Q70032	Q70032 streptomyc
299	8	2.3	820	2	Q9RQ11	Q9rqt1 streptococc	372	7	2.0	193	13	Q90WC7	Q90wc7 oncorhynch
300	8	2.3	836	7	Q8SNA3	Q8sna3 mus musculu	373	7	2.0	194	2	Q9L5B5	Q9l5b5 streptococc
301	8	2.3	860	5	Q9NDF9	Q9ndt9 balanus amp	374	7	2.0	194	13	Q90W49	Q90w49 decapteris
302	8	2.3	875	2	Q9F2B0	Q9f2b0 thibacillu	375	7	2.0	197	16	Q9L0F1	Q9l0f1 streptomyc
303	8	2.3	941	5	Q95TX9	Q95tx9 drosophila	376	7	2.0	200	10	Q9AX80	Q9ax80 oryza sativ
304	8	2.3	963	3	Q43024	Q43024 schizosacch	377	7	2.0	200	17	O58477	O58477 pyrococcus
305	8	2.3	1004	3	Q9HE23	Q9hez3 neurospora	378	7	2.0	204	3	O13598	O13598 schizosacch
306	8	2.3	1004	10	Q9L174	Q9l174 arabidopsis	379	7	2.0	204	10	O8S2Q1	O8szq1 oryza sativ
307	8	2.3	1015	5	Q9VY60	Q9vy60 drosophila	380	7	2.0	206	10	O9LVA5	O9lva5 arabidopsis
308	8	2.3	1023	4	Q92502	Q92502 homo sapien	381	7	2.0	207	10	O8L227	O8l227 arabidopsis

Q9p2x1 homo sapien
Q9fw41 oryza sativ
Q9nmr7 homo sapien
Q9o2t9 caenorhabdi
Q9wtm8 rattus norv
Q57580 gallus gall
Q921r2 mus musculu
Q9p422 neurospora
Q8t9f6 drosophila
Q8t4m0 drosophila
Q9vlq8 drosophila
Q8t4l8 drosophila
Q9sp10 drosophila
Q17970 caenorhabdi
Q9str0 drosophila
Q9jp78 bordetella
Q924c5 mus musculu
Q9v5j8 drosophila
Q8s789 oryza sativ
Q9vra6 drosophila
Q9g296 plasmodium
Q9jp78 bordetella
Q8xs40 raietonia s
Q9nw6 streptomyc
Q8w701 cyanohege
Q9f212 roseteles
Q8s0t1 oryza sativ
Q9w8v6 drosophila
Q8w6y8 cyanohege
Q9pxp5 hepatitis c
Q9pxp4 hepatitis c
Q9y9n3 aeropyrum p
Q945q3 arabidopsis
Q97222 sulfolobus
Q8x220 raietonia s
Q92b40 listeria in
Q9bdg2 bos taurus
Q9sra0 drosophila
Q40615 oryza rufip
Q9se04 oryza sativ
Q9zt17 arabidopsis
Q8r2r5 oryza sativ
Q9h4u5 homo sapien
Q8u303 pyrococcus
Q9zaa7 acidaminoco
Q07907 rhodobacter
Q8qnk4 ectocarpus
Q8xsu0 raietonia s
Q8tcg9 homo sapien
Q90w43 decapteris
Q9s268 osteria
Q9c684 arabidopsis
Q9ib38 thunnus thy
Q9d367 mus musculu
Q9shy3 arabidopsis
Q8sws3 drosophila
Q9fb14 streptomyc
Q9esu4 mus musculu
Q9d7t0 mus musculu
Q8szd3 drosophila
Q91792 xenopus lae
Q70032 streptomyc
Q90wc7 oncorhynch
Q9l5b5 streptococc
Q90w49 decapteris
Q9l0f1 streptomyc
Q9ax80 oryza sativ
O58477 pyrococcus
O13598 schizosacch
O8szq1 oryza sativ
O9lva5 arabidopsis
O8l227 arabidopsis

382	7	2.0	209	2	Q9L593	Q9L593 streptococc	455	7	2.0	318	17	Q8TRU1	Q8TRU1 methanosarc
383	7	2.0	209	10	Q9FPB2	Q9FPB2 arabisopsis	456	7	2.0	320	10	Q8S833	Q8S833 oryza sativ
384	7	2.0	210	16	Q8Z981	Q8Z981 salmonella	457	7	2.0	321	16	Q3L154	Q3L154 vibrio chol
385	7	2.0	211	12	Q9G9B7	Q9G9B7 culex nigri	458	7	2.0	323	11	Q9EQ24	Q9EQ24 rattus norv
386	7	2.0	211	12	Q9I909	Q9I909 culex nigri	459	7	2.0	323	11	Q9EQ22	Q9EQ22 rattus norv
387	7	2.0	212	10	Q9M208	Q9M208 arabisopsis	460	7	2.0	325	2	Q3X4R7	Q3X4R7 pseudomonas
388	7	2.0	212	12	Q4L1980	Q4L1980 murid herpe	461	7	2.0	325	2	Q9X4R8	Q9X4R8 pseudomonas
389	7	2.0	212	16	Q92KL1	Q92KL1 rhizobium m	462	7	2.0	327	10	Q9FWI9	Q9FWI9 oryza sativ
390	7	2.0	213	10	Q43600	Q43600 oryza sativ	463	7	2.0	328	3	Q9UR34	Q9UR34 schizosacch
391	7	2.0	215	4	Q9UNGO	Q9UNGO homo sapien	464	7	2.0	329	11	Q9JK33	Q9JK33 mus musculu
392	7	2.0	222	2	Q9L584	Q9L584 streptococc	465	7	2.0	331	4	Q16509	Q16509 homo sapien
393	7	2.0	222	10	Q9S740	Q9S740 arabisopsis	466	7	2.0	331	5	Q9V728	Q9V728 drosophila
394	7	2.0	223	5	Q9VV16	Q9VV16 drosophila	467	7	2.0	333	4	Q9NY94	Q9NY94 homo sapien
395	7	2.0	228	5	Q17275	Q17275 brugia paha	468	7	2.0	335	5	Q8S254	Q8S254 drosophila
396	7	2.0	228	10	Q8S0R0	Q8S0R0 oryza sativ	469	7	2.0	338	10	Q9S7K6	Q9S7K6 oryza sativ
397	7	2.0	231	5	Q9VXE4	Q9VXE4 drosophila	470	7	2.0	339	11	Q8RJ30	Q8RJ30 mus musculu
398	7	2.0	233	2	Q9L568	Q9L568 streptococc	471	7	2.0	345	4	Q96IH2	Q96IH2 homo sapien
399	7	2.0	236	2	Q9L569	Q9L569 streptococc	472	7	2.0	347	16	Q9RR94	Q9RR94 delinococcus
400	7	2.0	236	12	Q8S028	Q8S028 pseudorabie	473	7	2.0	348	16	Q9RTK5	Q9RTK5 delinococcus
401	7	2.0	236	16	Q92BG4	Q92BG4 listeria in	474	7	2.0	349	11	Q9ERM9	Q9ERM9 mus musculu
402	7	2.0	238	16	Q99006	Q99006 streptomyce	475	7	2.0	350	10	Q9FM99	Q9FM99 arabisopsis
403	7	2.0	239	10	Q94EG7	Q94EG7 arabisopsis	476	7	2.0	351	2	Q93TD8	Q93TD8 pseudomonas
404	7	2.0	242	2	Q9L562	Q9L562 streptococc	477	7	2.0	351	5	Q8SZ25	Q8SZ25 drosophila
405	7	2.0	242	10	Q8RF1	Q8RF1 oryza sativ	478	7	2.0	354	5	Q9VCN5	Q9VCN5 drosophila
406	7	2.0	243	2	Q9L567	Q9L567 streptococc	479	7	2.0	354	10	Q9ATT2	Q9ATT2 phacelurus
407	7	2.0	243	2	Q9L564	Q9L564 streptococc	480	7	2.0	354	16	Q8Z4E3	Q8Z4E3 salmonella
408	7	2.0	244	2	Q9L565	Q9L565 streptococc	481	7	2.0	355	10	Q9LE25	Q9LE25 chlamydomon
409	7	2.0	246	2	Q9L5B4	Q9L5B4 streptococc	482	7	2.0	356	16	Q8YAY7	Q8YAY7 brucella me
410	7	2.0	246	2	Q9L578	Q9L578 streptococc	483	7	2.0	356	17	Q8TG22	Q8TG22 methanopyru
411	7	2.0	246	10	Q9LVW8	Q9LVW8 arabisopsis	484	7	2.0	362	10	Q9ATS8	Q9ATS8 cymbopogon
412	7	2.0	247	2	Q9L566	Q9L566 streptococc	485	7	2.0	362	12	Q04325	Q04325 chicory yel
413	7	2.0	249	2	Q9L585	Q9L585 streptococc	486	7	2.0	365	16	Q9RUH9	Q9RUH9 delinococcus
414	7	2.0	249	2	Q9L570	Q9L570 streptococc	487	7	2.0	366	10	Q93339	Q93339 arabisopsis
415	7	2.0	249	5	Q8TA41	Q8TA41 heterodera	488	7	2.0	371	12	Q8V973	Q8V973 lily mottle
416	7	2.0	249	10	Q9FKJ8	Q9FKJ8 arabisopsis	489	7	2.0	374	2	Q9F0F7	Q9F0F7 campylobact
417	7	2.0	249	10	Q94J05	Q94J05 oryza sativ	490	7	2.0	375	16	Q9RW21	Q9RW21 delinococcus
418	7	2.0	249	16	Q9M222	Q9M222 rhizobium l	491	7	2.0	377	10	Q9FTN9	Q9FTN9 oryza sativ
419	7	2.0	251	16	Q98BC9	Q98BC9 rhizobium l	492	7	2.0	380	2	Q9S405	Q9S405 proteus mir
420	7	2.0	252	10	Q9S2U5	Q9S2U5 arabisopsis	493	7	2.0	380	11	Q9LWA6	Q9LWA6 mus musculu
421	7	2.0	254	2	Q9L563	Q9L563 streptococc	494	7	2.0	384	10	Q94DU1	Q94DU1 oryza sativ
422	7	2.0	255	2	Q9L5B6	Q9L5B6 streptococc	495	7	2.0	384	11	Q9D4D1	Q9D4D1 mus musculu
423	7	2.0	255	2	Q9L581	Q9L581 streptococc	496	7	2.0	388	5	Q9VMV9	Q9VMV9 drosophila
424	7	2.0	255	4	Q9H3S2	Q9H3S2 homo sapien	497	7	2.0	388	16	Q88027	Q88027 streptomyce
425	7	2.0	255	10	Q9LGM5	Q9LGM5 oryza sativ	498	7	2.0	390	5	Q9VAZ8	Q9VAZ8 drosophila
426	7	2.0	256	2	Q9L590	Q9L590 streptococc	499	7	2.0	393	17	Q9HJZ2	Q9HJZ2 thermoplasm
427	7	2.0	257	2	Q9L594	Q9L594 streptococc	500	7	2.0	393	2	Q9LAZ3	Q9LAZ3 streptococc
428	7	2.0	257	4	Q96J66	Q96J66 homo sapien	501	7	2.0	393	11	Q9JJF4	Q9JJF4 mus musculu
429	7	2.0	258	4	Q9BR67	Q9BR67 homo sapien	502	7	2.0	398	2	Q9RTM1	Q9RTM1 streptomyce
430	7	2.0	258	16	Q9K482	Q9K482 streptomyce	503	7	2.0	399	5	Q9VHA7	Q9VHA7 drosophila
431	7	2.0	259	16	Q92X87	Q92X87 rhizobium m	504	7	2.0	400	16	Q9ADJ6	Q9ADJ6 streptomyce
432	7	2.0	261	16	Q9JX72	Q9JX72 neisseria m	505	7	2.0	401	2	Q9LAZ2	Q9LAZ2 streptococc
433	7	2.0	262	16	Q9RTQ7	Q9RTQ7 delinococcus	506	7	2.0	404	10	Q9FGJ5	Q9FGJ5 arabisopsis
434	7	2.0	265	16	Q8YUV1	Q8YUV1 anabaena sp	507	7	2.0	404	12	Q9LFP26	Q9LFP26 cydia pomon
435	7	2.0	265	16	Q8UD55	Q8UD55 agrobacteri	508	7	2.0	405	16	Q92NK3	Q92NK3 rhizobium m
436	7	2.0	275	2	Q8RKD3	Q8RKD3 erwinia chr	509	7	2.0	407	10	Q9FRC8	Q9FRC8 oryza sativ
437	7	2.0	275	12	Q8V705	Q8V705 tulip band-	510	7	2.0	407	10	Q23555	Q23555 arabisopsis
438	7	2.0	278	12	Q83418	Q83418 pseudorabie	511	7	2.0	407	10	Q23555	Q23555 arabisopsis
439	7	2.0	278	16	Q9RL59	Q9RL59 streptomyce	512	7	2.0	409	3	Q8X0K2	Q8X0K2 neutrospora
440	7	2.0	279	10	Q9CAS2	Q9CAS2 arabisopsis	513	7	2.0	412	2	P95595	P95595 rhodobacter
441	7	2.0	282	16	Q8XMR7	Q8XMR7 clostridium	514	7	2.0	413	2	P56077	P56077 streptomyce
442	7	2.0	283	16	Q8XXN3	Q8XXN3 ralstonia s	515	7	2.0	416	2	Q33481	Q33481 psychrobact
443	7	2.0	286	2	Q9R640	Q9R640 mycobacteri	516	7	2.0	425	4	Q9NPN3	Q9NPN3 homo sapien
444	7	2.0	289	10	Q4L824	Q4L824 zea mays (m	517	7	2.0	425	17	Q9HPW5	Q9HPW5 halobacteri
445	7	2.0	290	16	Q99QA0	Q99QA0 streptomyce	518	7	2.0	426	16	Q8UHH4	Q8UHH4 agrobacteri
446	7	2.0	294	10	Q8WQ08	Q8WQ08 sorghum bic	519	7	2.0	428	16	Q9RIP5	Q9RIP5 streptococc
447	7	2.0	296	5	Q9V729	Q9V729 drosophila	520	7	2.0	430	16	Q8YR44	Q8YR44 anabaena sp
448	7	2.0	296	16	Q87L29	Q87L29 pseudomonas	521	7	2.0	431	10	Q8VZ63	Q8VZ63 arabisopsis
449	7	2.0	297	10	Q4L122	Q4L122 phaseolus v	522	7	2.0	434	10	Q8RWB6	Q8RWB6 arabisopsis
450	7	2.0	305	16	Q8XUP6	Q8XUP6 ralstonia s	523	7	2.0	435	10	Q9SUW1	Q9SUW1 arabisopsis
451	7	2.0	307	16	Q8UDS6	Q8UDS6 agrobacteri	524	7	2.0	437	4	Q9G2Q2	Q9G2Q2 homo sapien
452	7	2.0	310	16	Q8Y2T9	Q8Y2T9 ralstonia s	525	7	2.0	437	10	Q9FDW2	Q9FDW2 oryza sativ
453	7	2.0	314	10	Q8S750	Q8S750 oryza sativ	526	7	2.0	442	10	Q9LWR6	Q9LWR6 oryza sativ
454	7	2.0	317	4	Q96B32	Q96B32 homo sapien	527	7	2.0	445	4	Q96FB6	Q96FB6 homo sapien

528	7	2.0	449	12	Q86537	Q86537 tulip break	601	7	2.0	642	12	Q65846	Q65846 barley yell
529	7	2.0	450	12	Q8QNH5	Q8QNH5 ectocarpus	602	7	2.0	643	5	Q9XUT0	Q9XUT0 caenorhabdi
530	7	2.0	451	2	Q8657	Q8657 moraxella c	603	7	2.0	648	17	Q28883	Q28883 archaeglob
531	7	2.0	455	5	Q61747	Q61747 caenorhabdi	604	7	2.0	649	16	Q9CKD9	Q9CKD9 pasteurella
532	7	2.0	457	16	Q12650	Q12650 streptococ	605	7	2.0	652	11	Q9D2M6	Q9D2M6 mus musculu
533	7	2.0	460	12	Q12659	Q12659 apple chlor	606	7	2.0	662	10	Q9LTX1	Q9LTX1 arabidopsis
534	7	2.0	469	4	Q99492	Q99492 homo sapien	607	7	2.0	663	10	Q9FJ13	Q9FJ13 arabidopsis
535	7	2.0	470	2	Q9K3D7	Q9K3D7 moritella s	608	7	2.0	674	10	Q9C7B4	Q9C7B4 arabidopsis
536	7	2.0	475	5	Q9NGJ2	Q9NGJ2 drosophila	609	7	2.0	676	2	Q07365	Q07365 chlamydia t
537	7	2.0	475	5	Q9NGJ1	Q9NGJ1 drosophila	610	7	2.0	677	4	Q8TCL1	Q8TCL1 homo sapien
538	7	2.0	475	5	Q9NGJ0	Q9NGJ0 drosophila	611	7	2.0	683	4	Q8WV85	Q8WV85 homo sapien
539	7	2.0	475	5	Q9NGR2	Q9NGR2 drosophila	612	7	2.0	691	5	Q19243	Q19243 caenorhabdi
540	7	2.0	475	5	Q9NGE6	Q9NGE6 drosophila	613	7	2.0	700	16	Q9PFT1	Q9PFT1 xylella fas
541	7	2.0	475	5	Q9W2X5	Q9W2X5 drosophila	614	7	2.0	703	16	Q9PP16	Q9PP16 campylobact
542	7	2.0	479	2	Q9LAX2	Q9LAX2 streptococ	615	7	2.0	703	16	Q9P5F8	Q9P5F8 mus musculu
543	7	2.0	480	2	Q9LAX3	Q9LAX3 streptococ	616	7	2.0	716	11	Q8R5F8	Q8R5F8 mus musculu
544	7	2.0	481	2	Q9LAX5	Q9LAX5 streptococ	617	7	2.0	723	4	Q8T6E8	Q8T6E8 homo sapien
545	7	2.0	486	16	Q86746	Q86746 streptomyc	618	7	2.0	723	16	Q8VIR7	Q8VIR7 mycobacteri
546	7	2.0	487	16	Q8XRH4	Q8XRH4 ralstonia s	619	7	2.0	724	6	Q9MNO0	Q9MNO0 bos taurus
547	7	2.0	489	10	Q9SS90	Q9SS90 arabidopsis	620	7	2.0	726	11	Q924S6	Q924S6 mus musculu
548	7	2.0	494	10	Q9A8I4	Q9A8I4 oryza sativ	621	7	2.0	729	16	Q9G743	Q9G743 mycobacteri
549	7	2.0	495	16	Q9KVE4	Q9KVE4 streptomyc	622	7	2.0	733	4	Q9BZQ1	Q9BZQ1 homo sapien
550	7	2.0	502	2	Q9LAX8	Q9LAX8 streptomyc	623	7	2.0	739	3	Q9P683	Q9P683 neurospora
551	7	2.0	508	16	Q9F2X3	Q9F2X3 streptomyc	624	7	2.0	743	16	Q9L0S2	Q9L0S2 streptomyc
552	7	2.0	512	5	Q9VM14	Q9VM14 drosophila	625	7	2.0	745	4	Q9P2N8	Q9P2N8 homo sapien
553	7	2.0	513	3	Q9C1X4	Q9C1X4 schizosacch	626	7	2.0	757	16	Q98QH0	Q98QH0 mycoplasma
554	7	2.0	515	2	Q9L8T0	Q9L8T0 treponema p	627	7	2.0	757	17	Q8TIV7	Q8TIV7 methanosarc
555	7	2.0	516	2	Q9L8T3	Q9L8T3 treponema p	628	7	2.0	758	10	Q9C838	Q9C838 arabidopsis
556	7	2.0	519	2	Q9K820	Q9K820 streptococ	629	7	2.0	759	12	Q8UYT2	Q8UYT2 lily mottle
557	7	2.0	524	12	Q83417	Q83417 pseudorabie	630	7	2.0	772	17	Q8U3U2	Q8U3U2 pyrococcus
558	7	2.0	524	16	Q8RYI0	Q8RYI0 deinococcus	631	7	2.0	784	16	Q8XS28	Q8XS28 ralstonia s
559	7	2.0	526	12	Q85027	Q85027 pseudorabie	632	7	2.0	786	16	Q8XPV8	Q8XPV8 ralstonia s
560	7	2.0	528	2	Q03536	Q03536 escherichia	633	7	2.0	787	3	Q94096	Q94096 pneumococci
561	7	2.0	532	10	Q9FWD7	Q9FWD7 oryza sativ	634	7	2.0	801	5	Q9GRL1	Q9GRL1 leishmania
562	7	2.0	538	16	Q8RI12	Q8RI12 fusobacteri	635	7	2.0	809	16	Q8X224	Q8X224 ralstonia s
563	7	2.0	540	12	Q93711	Q93711 cercopithe	636	7	2.0	811	5	Q9VT40	Q9VT40 drosophila
564	7	2.0	541	16	Q9RDH9	Q9RDH9 streptomyc	637	7	2.0	811	16	Q9X8T0	Q9X8T0 streptomyc
565	7	2.0	547	10	Q94GC1	Q94GC1 oryza sativ	638	7	2.0	816	4	Q9G551	Q9G551 homo sapien
566	7	2.0	551	16	Q9H0D4	Q9H0D4 pseudomonas	639	7	2.0	824	4	Q8TEK9	Q8TEK9 homo sapien
567	7	2.0	556	5	Q95RC6	Q95RC6 drosophila	640	7	2.0	826	10	Q940X9	Q940X9 arabidopsis
568	7	2.0	556	16	Q53678	Q53678 mycobacteri	641	7	2.0	833	16	Q8YUW6	Q8YUW6 anabaena sp
569	7	2.0	557	5	Q23933	Q23933 drosophila	642	7	2.0	845	5	Q9GRL1	Q9GRL1 leishmania
570	7	2.0	566	11	Q9ER03	Q9ER03 mus musculu	643	7	2.0	852	11	Q8R077	Q8R077 mus musculu
571	7	2.0	568	16	Q9RWU8	Q9RWU8 deinococcus	644	7	2.0	854	11	Q54971	Q54971 mus musculu
572	7	2.0	569	6	Q28616	Q28616 oryctolagus	645	7	2.0	855	4	Q8WTX5	Q8WTX5 homo sapien
573	7	2.0	570	2	Q9APH1	Q9APH1 leptospira	646	7	2.0	855	17	Q8TTP9	Q8TTP9 methanosarc
574	7	2.0	574	3	Q36027	Q36027 schizosacch	647	7	2.0	857	16	Q98IK2	Q98IK2 schizosacch
575	7	2.0	574	5	Q17411	Q17411 aedes aegypt	648	7	2.0	862	4	Q9BY75	Q9BY75 homo sapien
576	7	2.0	574	16	Q9RTJ3	Q9RTJ3 deinococcus	649	7	2.0	870	3	Q8W2W3	Q8W2W3 neurospora
577	7	2.0	576	5	Q9WX72	Q9WX72 drosophila	650	7	2.0	884	4	Q00302	Q00302 homo sapien
578	7	2.0	580	4	Q96ID0	Q96ID0 homo sapien	651	7	2.0	884	4	Q8WU30	Q8WU30 homo sapien
579	7	2.0	584	16	Q9FCJ3	Q9FCJ3 streptomyc	652	7	2.0	903	4	Q96F66	Q96F66 homo sapien
580	7	2.0	586	10	Q40643	Q40643 oryza sativ	653	7	2.0	907	16	Q8Y260	Q8Y260 anabaena sp
581	7	2.0	586	16	Q9L0T7	Q9L0T7 streptomyc	654	7	2.0	913	16	Q8UJ51	Q8UJ51 agrobacteri
582	7	2.0	587	10	Q23241	Q23241 arabidopsis	655	7	2.0	923	6	Q97745	Q97745 sus scrofa
583	7	2.0	587	16	Q9HUC8	Q9HUC8 pseudomonas	656	7	2.0	931	4	Q969V6	Q969V6 homo sapien
584	7	2.0	587	16	Q9F4K5	Q9F4K5 caulobacter	657	7	2.0	932	5	Q01623	Q01623 caenorhabdi
585	7	2.0	588	10	Q948Y3	Q948Y3 oryza sativ	658	7	2.0	934	4	Q9P2B0	Q9P2B0 homo sapien
586	7	2.0	589	4	Q75148	Q75148 homo sapien	659	7	2.0	938	3	Q96V14	Q96V14 pneumococci
587	7	2.0	590	5	Q8SSB8	Q8SSB8 encephalito	660	7	2.0	942	5	Q8WRX5	Q8WRX5 anopheles g
588	7	2.0	594	2	Q95099	Q95099 alcaligenes	661	7	2.0	945	6	Q77589	Q77589 equus cabal
589	7	2.0	594	5	Q9VEP4	Q9VEP4 drosophila	662	7	2.0	948	6	Q9T7D7	Q9T7D7 trichosurus
590	7	2.0	596	4	Q9NXH0	Q9NXH0 homo sapien	663	7	2.0	954	5	Q95XZ3	Q95XZ3 leishmania
591	7	2.0	596	11	Q96BB7	Q96BB7 mus musculu	664	7	2.0	954	13	Q91909	Q91909 xenopus lae
592	7	2.0	596	16	Q8YUW8	Q8YUW8 ralstonia s	665	7	2.0	964	6	Q97744	Q97744 sus scrofa
593	7	2.0	600	16	Q8YUW8	Q8YUW8 streptomyc	666	7	2.0	964	6	Q9TQ01	Q9TQ01 sus scrofa
594	7	2.0	606	4	Q9NPU0	Q9NPU0 homo sapien	667	7	2.0	964	6	Q9TQ00	Q9TQ00 sus scrofa
595	7	2.0	622	12	Q8V972	Q8V972 lily mottle	668	7	2.0	972	4	Q99662	Q99662 homo sapien
596	7	2.0	626	3	Q9HFV3	Q9HFV3 ashbya goss	669	7	2.0	974	2	Q9S0V6	Q9S0V6 streptomyc
597	7	2.0	629	2	Q9K3D6	Q9K3D6 moritella s	670	7	2.0	974	11	Q63702	Q63702 rattus ratt
598	7	2.0	629	6	Q29426	Q29426 oryctolagus	671	7	2.0	974	13	Q985U3	Q985U3 danio dangi
599	7	2.0	636	16	Q8U9F8	Q8U9F8 agrobacteri	672	7	2.0	975	13	P9750	P9750 fugu rubrip
600	7	2.0	640	16	Q06293	Q06293 mycobacteri	673	7	2.0	977	13	Q918N6	Q918N6 brachydanio

674	7	2.0	977	13	Q98SU4	Q98su4 danio alb	747	6	1.7	66	11	Q91WH0	Q91wh0 mus musculu
675	7	2.0	977	13	Q98SU1	Q98su1 danio nigro	748	6	1.7	67	10	Q91WH0	Q91wh0 mus musculu
676	7	2.0	978	6	Q9XS93	Q9xs93 canis fami	749	6	1.7	67	10	Q9XS93	Q9xs93 canis fami
677	7	2.0	978	11	Q63116	Q63116 rattus norv	750	6	1.7	67	16	Q9KDS3	Q9kds3 bacillus ha
678	7	2.0	979	6	Q8WN23	Q8wn23 canis fami	751	6	1.7	68	2	Q83015	Q83015 streptomyce
679	7	2.0	995	11	Q35615	Q35615 mus musculu	752	6	1.7	68	16	Q9K805	Q9k805 bacillus ha
680	7	2.0	1006	3	Q9C244	Q9c244 neurospora	753	6	1.7	69	8	Q31945	Q31945 cheno
681	7	2.0	1021	2	Q9K516	Q9k516 actinoplane	754	6	1.7	69	10	Q94DB9	Q94db9 oryza sativ
682	7	2.0	1039	5	Q9VW88	Q9vw88 drosophila	755	6	1.7	70	5	Q16428	Q16428 caenorhabdi
683	7	2.0	1053	4	Q96KJ4	Q96kj4 homo sapien	756	6	1.7	70	5	Q98KA0	Q98ka0 rhizobium l
684	7	2.0	1087	5	Q26156	Q26156 plasmodium	757	6	1.7	70	16	Q98KA0	Q98ka0 rhizobium l
685	7	2.0	1095	5	Q9U4G4	Q9u4g4 drosophila	758	6	1.7	72	5	Q9V6H0	Q9v6h0 drosophila
686	7	2.0	1111	16	Q8E522	Q8e522 streptomyce	759	6	1.7	73	5	Q9V6H0	Q9v6h0 drosophila
687	7	2.0	1132	16	Q9RRC7	Q9rrc7 deinococcus	760	6	1.7	73	16	Q9PAD1	Q9pad1 arabidopsis
688	7	2.0	1149	5	Q23315	Q23315 caenorhabdi	761	6	1.7	73	16	Q9PAD1	Q9pad1 arabidopsis
689	7	2.0	1158	4	Q14113	Q14113 homo sapien	762	6	1.7	73	16	Q9XV9	Q9xv9 talstonia s
690	7	2.0	1172	5	Q9G210	Q9g210 caenorhabdi	763	6	1.7	74	12	Q9YJ8	Q9yj8 hepatitis c
691	7	2.0	1264	5	Q91767	Q91767 manduca sex	764	6	1.7	74	12	Q9YJ8	Q9yj8 hepatitis c
692	7	2.0	1272	16	Q9UM53	Q9um53 streptomyce	765	6	1.7	74	12	Q9YJ8	Q9yj8 hepatitis c
693	7	2.0	1274	4	Q9UM53	Q9um53 homo sapien	766	6	1.7	74	12	Q9YJ8	Q9yj8 hepatitis c
694	7	2.0	1312	4	Q9COC9	Q9coc9 homo sapien	767	6	1.7	74	12	Q9YJ8	Q9yj8 hepatitis c
695	7	2.0	1313	4	Q9COC9	Q9coc9 homo sapien	768	6	1.7	74	12	Q9YJ8	Q9yj8 hepatitis c
696	7	2.0	1343	4	Q9H7N4	Q9h7n4 homo sapien	769	6	1.7	74	12	Q9YJ8	Q9yj8 hepatitis c
697	7	2.0	1406	4	Q9Y216	Q9y216 homo sapien	770	6	1.7	74	12	Q9YJ8	Q9yj8 hepatitis c
698	7	2.0	1464	5	Q24132	Q24132 drosophila	771	6	1.7	74	12	Q9YJ8	Q9yj8 hepatitis c
699	7	2.0	1464	5	Q23395	Q23395 drosophila	772	6	1.7	74	12	Q9YJ8	Q9yj8 hepatitis c
700	7	2.0	1464	5	Q9VC47	Q9vc47 drosophila	773	6	1.7	74	12	Q9YJ8	Q9yj8 hepatitis c
701	7	2.0	1663	4	Q9UQ01	Q9uq01 homo sapien	774	6	1.7	74	12	Q9YJ8	Q9yj8 hepatitis c
702	7	2.0	1693	5	Q9W3P3	Q9w3p3 drosophila	775	6	1.7	75	5	Q9U316	Q9u316 caenorhabdi
703	7	2.0	1711	5	Q95YX3	Q95yx3 leishmania	776	6	1.7	75	5	Q9U316	Q9u316 caenorhabdi
704	7	2.0	1714	10	Q94HT9	Q94ht9 oryza sativ	777	6	1.7	77	5	Q9N822	Q9n822 trypanosoma
705	7	2.0	1766	5	Q25668	Q25668 plasmodium	778	6	1.7	77	16	Q9XV9	Q9xv9 talstonia s
706	7	2.0	1777	10	Q94HP9	Q94hp9 oryza sativ	779	6	1.7	79	2	Q9XV9	Q9xv9 talstonia s
707	7	2.0	1819	10	Q8SA24	Q8sa24 oryza sativ	780	6	1.7	79	16	Q9XV9	Q9xv9 talstonia s
708	7	2.0	1883	4	Q96SC5	Q96sc5 homo sapien	781	6	1.7	79	16	Q9XV9	Q9xv9 talstonia s
709	7	2.0	1905	4	Q96SC5	Q96sc5 homo sapien	782	6	1.7	79	16	Q9XV9	Q9xv9 talstonia s
710	7	2.0	1929	5	Q95YQ9	Q95yq9 leishmania	783	6	1.7	80	2	Q93B65	Q93b65 salmonella
711	7	2.0	2146	3	Q95R97	Q95r97 leishmania	784	6	1.7	80	2	Q93B65	Q93b65 salmonella
712	7	2.0	2146	3	Q60026	Q60026 aspergillus	785	6	1.7	82	2	Q93B28	Q93b28 salmonella
713	7	2.0	2209	5	Q97324	Q97324 plasmodium	786	6	1.7	82	2	Q93B28	Q93b28 salmonella
714	7	2.0	2408	5	Q22184	Q22184 plasmodium	787	6	1.7	82	2	Q93B28	Q93b28 salmonella
715	7	2.0	2592	3	Q9F3J0	Q9f3j0 neurospora	788	6	1.7	82	16	Q9RSW2	Q9rsw2 deinococcus
716	7	2.0	2592	3	Q9F3J0	Q9f3j0 neurospora	789	6	1.7	82	16	Q9RSW2	Q9rsw2 deinococcus
717	7	2.0	3192	2	Q914W4	Q914w4 streptomyce	790	6	1.7	83	2	Q93AW8	Q93aw8 salmonella
718	7	2.0	3247	12	Q65593	Q65593 bovine herp	791	6	1.7	83	2	Q93AW8	Q93aw8 salmonella
719	7	2.0	3361	4	Q9V556	Q9v556 bovine herp	792	6	1.7	83	2	Q93AW8	Q93aw8 salmonella
720	7	2.0	3361	4	Q9V556	Q9v556 bovine herp	793	6	1.7	83	2	Q93AW8	Q93aw8 salmonella
721	7	2.0	3361	4	Q9V556	Q9v556 bovine herp	794	6	1.7	83	2	Q93AW8	Q93aw8 salmonella
722	7	2.0	3361	4	Q9V556	Q9v556 bovine herp	795	6	1.7	83	2	Q93AW8	Q93aw8 salmonella
723	7	2.0	3664	4	Q96T58	Q96t58 drosophila	796	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
724	7	2.0	5644	2	Q93NX8	Q93nx8 homo sapien	797	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
725	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	798	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
726	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	799	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
727	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	800	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
728	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	801	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
729	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	802	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
730	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	803	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
731	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	804	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
732	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	805	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
733	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	806	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
734	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	807	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
735	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	808	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
736	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	809	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
737	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	810	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
738	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	811	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
739	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	812	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
740	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	813	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
741	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	814	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
742	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	815	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
743	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	816	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
744	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	817	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
745	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	818	6	1.7	84	2	Q93B43	Q93b43 mycobacteri
746	6	1.7	5990	2	Q9RLP6	Q9rlp6 streptomyce	819	6	1.7	84	2	Q93B43	Q93b43 mycobacteri

820	1.7	97	10	Q9FTN1	Q9ftn1 oryza sativ	893	6	1.7	115	8	Q9MJJ4	Q9mj14 carabus gen
821	1.7	98	2	Q93B71	Q93b71 salmonella	894	6	1.7	115	8	Q9MJJ3	Q9mj13 carabus coa
822	1.7	98	2	Q93B10	Q93b10 salmonella	895	6	1.7	115	8	Q9MJJ2	Q9mj12 carabus abb
823	1.7	98	5	Q9VRG2	Q9vrg2 drosophila	896	6	1.7	115	8	Q9MJJ1	Q9mj11 carabus can
824	1.7	98	17	Q82W27	Q82w27 pyrobaculum	897	6	1.7	115	8	Q9MJJ0	Q9mj10 carabus aur
825	1.7	99	2	Q68434	Q68434 leptospira	898	6	1.7	115	8	Q9MJJ9	Q9mj19 carabus arv
826	1.7	99	2	Q68436	Q68436 leptospira	899	6	1.7	115	16	Q8XHD6	Q8xhd6 clostridium
827	1.7	100	2	Q93B57	Q93b57 salmonella	900	6	1.7	115	16	Q8XGE0	Q8xge0 salmonella
828	1.7	100	2	Q93AV9	Q93av9 salmonella	901	6	1.7	116	2	Q93B23	Q93b23 salmonella
829	1.7	100	10	Q9SWS7	Q9sWS7 arabidopsis	902	6	1.7	116	8	Q21026	Q21026 carabus pia
830	1.7	101	2	Q93B44	Q93b44 salmonella	903	6	1.7	116	8	Q21022	Q21022 carabus mel
831	1.7	101	12	Q93IAN2	Q93ian2 hepatitis b	904	6	1.7	116	8	Q21835	Q21835 carabus rug
832	1.7	102	2	Q93AW5	Q93aw5 salmonella	905	6	1.7	116	8	Q21751	Q21751 carabus int
833	1.7	103	2	Q93B52	Q93b52 salmonella	906	6	1.7	116	8	Q21847	Q21847 carabus mel
834	1.7	103	2	Q93AV3	Q93av3 salmonella	907	6	1.7	116	10	Q94E04	Q94e04 oryza sativ
835	1.7	104	2	Q93PB6	Q93pb6 microscilla	908	6	1.7	117	11	Q9D2C1	Q9d2c1 mus musculus
836	1.7	104	2	Q93AZ9	Q93az9 salmonella	909	6	1.7	118	5	Q9NE05	Q9ne05 caenorhabdi
837	1.7	104	10	Q9LUPV3	Q9lupv3 arabidopsis	910	6	1.7	118	16	Q8ZE70	Q8ze70 yersinia pe
838	1.7	104	16	Q8YR36	Q8yr36 anabaena sp	911	6	1.7	118	17	Q8ZE66	Q8ze66 sulfolobus
839	1.7	104	17	Q9HL12	Q9hl12 thermoplasma	912	6	1.7	119	12	Q67867	Q67867 hepatitis b
840	1.7	105	2	Q9AN17	Q9an17 bradyrhizob	913	6	1.7	119	12	Q91U87	Q91u87 hepatitis b
841	1.7	105	2	Q93B67	Q93b67 salmonella	914	6	1.7	119	12	Q91U86	Q91u86 hepatitis b
842	1.7	105	2	Q93B63	Q93b63 salmonella	915	6	1.7	119	12	Q91U85	Q91u85 hepatitis b
843	1.7	105	2	Q93B62	Q93b62 salmonella	916	6	1.7	119	16	Q8XAG6	Q8xag6 escherichia
844	1.7	105	2	Q93AX9	Q93ax9 salmonella	917	6	1.7	119	16	Q9L103	Q9l103 streptomyce
845	1.7	105	5	Q9N456	Q9n456 caenorhabdi	918	6	1.7	120	2	Q93AW2	Q93aw2 salmonella
846	1.7	106	8	Q9G744	Q9g744 convoluta c	919	6	1.7	120	3	Q14393	Q14393 schizosacch
847	1.7	107	2	Q93B73	Q93b73 salmonella	920	6	1.7	120	16	Q9RY81	Q9ry81 deinococcus
848	1.7	107	2	Q93B38	Q93b38 salmonella	921	6	1.7	121	2	Q93AV7	Q93av7 salmonella
849	1.7	107	2	Q93Q03	Q93q03 salmonella	922	6	1.7	121	10	Q9C8N8	Q9c8n8 arabidopsis
850	1.7	107	16	Q9ADC4	Q9adc4 streptomyce	923	6	1.7	122	5	Q9VVZ5	Q9vvz5 drosophila
851	1.7	108	2	Q93B78	Q93b78 salmonella	924	6	1.7	122	8	Q9MKM6	Q9mkM6 carabus abb
852	1.7	108	6	Q9XST8	Q9xst8 canis famli	925	6	1.7	122	8	Q9T279	Q9t279 carabus spl
853	1.7	108	10	Q9FVY4	Q9fvy4 oryza sativ	926	6	1.7	122	10	P93309	P93309 arabidopsis
854	1.7	108	10	Q94CY1	Q94cy1 oryza sativ	927	6	1.7	122	16	Q8XF39	Q8xf39 salmonella
855	1.7	108	16	Q9SS54	Q9ss54 staphylococ	928	6	1.7	123	2	Q93B70	Q93b70 salmonella
856	1.7	108	16	Q9CE28	Q9ce28 lactococcus	929	6	1.7	123	2	Q93AW9	Q93aw9 salmonella
857	1.7	109	2	Q93B61	Q93b61 salmonella	930	6	1.7	123	16	Q8ZJ17	Q8zj17 yersinia pe
858	1.7	109	5	Q9VV10	Q9vv10 drosophila	931	6	1.7	123	17	Q29448	Q29448 archaeoglob
859	1.7	109	10	Q8W5F8	Q8w5f8 oryza sativ	932	6	1.7	124	2	Q93SB7	Q93sb7 frankia sp.
860	1.7	109	12	Q81298	Q81298 hepatitis c	933	6	1.7	124	2	Q93GL2	Q93gl2 frankia sp.
861	1.7	109	12	Q81300	Q81300 hepatitis c	934	6	1.7	124	2	Q93B01	Q93b01 salmonella
862	1.7	109	12	Q81452	Q81452 hepatitis c	935	6	1.7	124	12	Q9QME9	Q9qme9 norwalk-lik
863	1.7	109	12	Q81459	Q81459 hepatitis c	936	6	1.7	124	16	Q9PG56	Q9pg56 xylella fas
864	1.7	109	12	Q81301	Q81301 hepatitis c	937	6	1.7	124	15	Q8R989	Q8r989 thermoanaer
865	1.7	109	12	Q81543	Q81543 hepatitis c	938	6	1.7	125	2	Q93M11	Q93m11 streptomyce
866	1.7	109	12	Q81482	Q81482 hepatitis c	939	6	1.7	125	2	Q93AZ7	Q93az7 salmonella
867	1.7	109	12	Q81545	Q81545 hepatitis c	940	6	1.7	125	2	Q93AZ4	Q93az4 salmonella
868	1.7	109	12	Q81802	Q81802 hepatitis c	941	6	1.7	125	12	Q91AP1	Q91ap1 hepatitis b
869	1.7	109	12	Q81804	Q81804 hepatitis c	942	6	1.7	125	12	Q91AP0	Q91ap0 hepatitis b
870	1.7	109	17	Q30024	Q30024 archaeoglob	943	6	1.7	125	12	Q91AN9	Q91an9 hepatitis b
871	1.7	110	2	Q93B55	Q93b55 salmonella	944	6	1.7	125	12	Q91AN7	Q91an7 hepatitis b
872	1.7	110	2	Q93B14	Q93b14 salmonella	945	6	1.7	125	12	Q91AN6	Q91an6 hepatitis b
873	1.7	110	2	Q933C1	Q933c1 salmonella	946	6	1.7	125	12	Q91AN5	Q91an5 hepatitis b
874	1.7	110	12	Q9DMK2	Q9dmk2 hepatitis c	947	6	1.7	125	12	Q91AN4	Q91an4 hepatitis b
875	1.7	111	2	Q93B77	Q93b77 salmonella	948	6	1.7	125	12	Q91AN3	Q91an3 hepatitis b
876	1.7	111	2	Q93B03	Q93b03 salmonella	949	6	1.7	125	12	Q91AN1	Q91an1 hepatitis b
877	1.7	111	8	Q9WJ17	Q9wj17 campalita m	950	6	1.7	125	12	Q91AN0	Q91an0 hepatitis b
878	1.7	111	12	Q67928	Q67928 hepatitis b	951	6	1.7	125	12	Q91AM9	Q91am9 hepatitis b
879	1.7	111	12	Q67940	Q67940 hepatitis b	952	6	1.7	125	16	Q9RRH9	Q9rrh9 deinococcus
880	1.7	111	12	Q67931	Q67931 hepatitis b	953	6	1.7	126	2	Q93B59	Q93b59 salmonella
881	1.7	112	2	Q93B42	Q93b42 salmonella	954	6	1.7	126	2	Q93B31	Q93b31 salmonella
882	1.7	112	2	Q93B00	Q93b00 salmonella	955	6	1.7	126	2	Q93B17	Q93b17 salmonella
883	1.7	113	10	Q92NXX2	Q92nx2 petunia hyb	956	6	1.7	126	2	Q93AZ3	Q93az3 salmonella
884	1.7	114	2	Q93B72	Q93b72 salmonella	957	6	1.7	126	10	Q9ZT18	Q9zt18 arabidopsis
885	1.7	114	2	Q93B13	Q93b13 salmonella	958	6	1.7	126	16	Q9FBX3	Q9fbx3 streptomyce
886	1.7	114	2	Q93AZ6	Q93az6 salmonella	959	6	1.7	127	2	Q54743	Q54743 streptococ
887	1.7	114	2	Q93AZ5	Q93az5 salmonella	960	6	1.7	127	2	Q93B79	Q93b79 salmonella
888	1.7	114	15	Q39132	Q39132 human immun	961	6	1.7	127	2	Q93B30	Q93b30 salmonella
889	1.7	115	2	Q93B27	Q93b27 salmonella	962	6	1.7	127	17	Q8ZSW8	Q8zsw8 pyrobaculum
890	1.7	115	2	Q93AX1	Q93ax1 salmonella	963	6	1.7	128	2	Q93AX0	Q93ax0 salmonella
891	1.7	115	8	Q9TK97	Q9tk97 kochia scop	964	6	1.7	128	10	Q9MAW0	Q9maw0 bruguliera g
892	1.7	115	8	Q9MJJ7	Q9mj17 carabus nit	965	6	1.7	128	10	Q9MAW0	Q9maw0 bruguliera g


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966 10 128 10 09L124
967 128 10 0943D8
968 129 2 093B80
969 129 2 093B80
970 129 2 093B80
971 129 2 093B32
972 129 2 093AY4
973 129 2 093AW6
974 129 16 09YWM4
975 130 2 093B68
976 130 2 0933S8
977 130 10 040603
978 131 2 093B04
979 131 2 093AW7
980 131 5 09V27
981 131 10 09SVJ7
982 131 12 040906
983 132 2 09EY79
984 132 2 093B75
985 132 2 093B56
986 132 2 093A28
987 132 8 099990
988 132 12 09VTK2
989 133 12 0805F8
990 134 2 093B37
991 134 2 093AX3
992 134 2 093B47
993 135 2 093B47
994 135 16 093B47
995 136 16 093B47
996 137 2 068058
997 137 2 09AGJ8
998 138 2 09F6Y0
999 138 2 093B54
1000 138 2 093AY2
1001 138 16 092A17
1002 138 16 09F5Q9

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Q91124 pinus taeda
Q943D8 oryza sativ
Q93B80 salmonella
Q93B48 salmonella
Q93B32 salmonella
Q93AY4 salmonella
Q93AW6 salmonella
Q9YWM4 anabaena sp
Q93B68 salmonella
Q933S8 salmonella
Q40603 oryza longi
Q05839 mycobacteri
Q93B04 salmonella
Q93AW7 salmonella
Q9V27 drosophila
Q9SVJ7 arabidopsis
Q40906 gallid herp
Q9EY79 pseudomonas
Q93B75 salmonella
Q93B56 salmonella
Q93A28 salmonella
Q99990 porphyra pu
Q9VTK2 ateline her
Q805F8 hepatitis b
Q93B37 salmonella
Q93AX3 salmonella
Q93B47 salmonella
P72919 synchocyst
068058 rhodobacter
Q9AGJ8 corynebacte
Q9F6Y0 chloroflexu
Q93B54 salmonella
Q93AY2 salmonella
Q92A17 listeria in
Q9F5Q9 listeria mo

ALIGNMENTS

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RESULT 1
Q99114
ID Q99114 PRELIMINARY; PRT; 238 AA.
AC Q99114;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Outer membrane protein A (Outer membrane protein II) (Fragment).
GN OMPA.
OS Escherichia vulneris.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29943;
RA MEDLINE=92065252; PubMed=1955870;
RA Lawrence J.G., Ochman H., Hartl D.L.;
RT "Molecular and evolutionary relationships among enteric bacteria.";
CC -I- SUBCELLULAR LOCATION: OUTER MEMBRANE.
DR ENBL; M63348; AAA24233.1;
DR HSSP; P02934; IQJP.
DR InterPro; IPR001145; Bac_OmpA.
DR InterPro; IPR000498; OmpA_tmemb.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01021; OmpA_membrane; 1.
DR PRODOM; PD000930; Bac_OmpA; 1.
DR PROSITE; PS01068; OMPA; 1.
KW Outer membrane; Porin; Phage recognition.
FT NON_TER 1
FT NON_TER 238

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SQ SEQUENCE 238 AA; 25604 MW; B05D116C01DD9733 CRC64;
Query Match 15.4%; Score 53; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 3.3e-45;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 213 FTLKSDVLFNFNFKATLKPEGQALDQLYTQLSNMDPKDGSVVVGLGYTDRIGSE 265
Db 116 FTLKSDVLFNFNFKATLKPEGQALDQLYTQLSNMDPKDGSVVVGLGYTDRIGSE 168
RESULT 2
Q99123
ID Q99123 PRELIMINARY; PRT; 238 AA.
AC Q99123;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Outer membrane protein A (Outer membrane protein II) (Fragment)
DE (Version 2).
GN OMPA.
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_TaxID=548;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E482;
RA MEDLINE=92065252; PubMed=1955870;
RA Lawrence J.G., Ochman H., Hartl D.L.;
RT "Molecular and evolutionary relationships among enteric bacteria.";
CC -I- SUBCELLULAR LOCATION: OUTER MEMBRANE.
DR ENBL; M63356; AAA24807.1;
DR HSSP; P02934; IQJP.
DR InterPro; IPR001145; Bac_OmpA.
DR InterPro; IPR000498; OmpA_tmemb.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01021; OmpA_membrane; 1.
DR PRODOM; PD000930; Bac_OmpA; 1.
DR PROSITE; PS01068; OMPA; 1.
KW Outer membrane; Porin; Phage recognition.
FT NON_TER 1
FT NON_TER 238
SQ SEQUENCE 238 AA; 25553 MW; BCD6AF25240202B CRC64;
Query Match 10.5%; Score 36; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 6e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 210 TKHFTLKSDVLFNFNFKATLKPEGQALDQLYTQLSN 245
Db 113 TKHFTLKSDVLFNFNFKATLKPEGQALDQLYTQLSN 148
RESULT 3
Q93QP1
ID Q93QP1 PRELIMINARY; PRT; 148 AA.
AC Q93QP1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMPA.
OS Erwinia persicina.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=55211;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=33998;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;

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Allelic diversity of the major outer membrane protein (OmpA) gene among necrogenic phytopathogenic species: Molecular evolutionary aspects of relatedness.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF220801: AAK68967.1; -;
 DR InterPro: IPR001145; Bac_OmpA.
 DR InterPro: IPR000498; OmpA_tmern.
 DR Pfam: PF00691; OmpA; 1.
 DR Pfam: PF01389; OmpA_membrane; 1.
 DR ProDom: PD000930; Bac_OmpA; 1.
 FT NON_TER 1 148
 FT NON_TER 148 148
 SQ SEQUENCE 148 AA; 16041 MW; 4124208BD384FCC1 CRC64;

Query Match 9.6%; Score 33; DB 2; Length 148;
 Best Local Similarity 100.0%; Pred. No. 4.2e-25;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 FTLSKSVLNFNFKATLKPEGQALDQYLTQLSN 245
 Db 107 FTLSKSVLNFNFKATLKPEGQALDQYLTQLSN 139

RESULT 4
 Q9L618 PRELIMINARY; PRT; 246 AA.
 AC Q9L618;
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Outer membrane protein A (Fragment).
 GN OMPA.

OS Shigella flexneri.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Shigella.
 OX NCBI_TaxID=623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang Y., Kim K.S.;
 RT "Structural and functional roles of OmpA in stress survival and invasion of brain microvascular endothelial cells in Escherichia coli.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF224271; AAF37889.1; -;
 DR HSSP: P02934; IQJP.
 DR InterPro: IPR001145; Bac_OmpA.
 DR InterPro: IPR000498; OmpA_tmern.
 DR Pfam: PF00691; OmpA; 1.
 DR Pfam: PF01389; OmpA_membrane; 1.
 FT NON_TER 246 246
 SQ SEQUENCE 246 AA; 26371 MW; 56C6D6225E6F079F CRC64;

Query Match 9.6%; Score 33; DB 2; Length 246;
 Best Local Similarity 100.0%; Pred. No. 6.9e-25;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 KAQGVQLTAKLGYPITDLDIYTRLGGMVWRAD 119
 Db 94 KAQGVQLTAKLGYPITDLDIYTRLGGMVWRAD 126

RESULT 5
 Q47880 PRELIMINARY; PRT; 244 AA.
 AC Q47880;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Outer membrane protein II (Fragment).
 GN OMPA.

OS Escherichia vulneris.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.

OX NCBI_TaxID=566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92065252; PubMed-1955870;
 RA Lawrence J.G., Ochman H., Hartl D.L.;
 RT "Molecular and evolutionary relationships among enteric bacteria.";
 RL J. Gen. Microbiol. 137:1911-1921(1991).
 DR EMBL: M63350; AAA24237.1; -;
 DR HSSP: P02934; IQJP.
 DR InterPro: IPR001145; Bac_OmpA.
 DR InterPro: IPR000498; OmpA_tmern.
 DR Pfam: PF00691; OmpA; 1.
 DR Pfam: PF01389; OmpA_membrane; 1.
 DR PRINTS: PR01021; OMPADOMAIN.
 DR ProDom: PD000930; Bac_OmpA; 1.
 DR PROSITE: PS01068; OmpA; 1.
 FT NON_TER 1 244
 FT NON_TER 244 244
 SQ SEQUENCE 244 AA; 26275 MW; C6D068A6A0916179 CRC64;

Query Match 8.4%; Score 29; DB 2; Length 244;
 Best Local Similarity 100.0%; Pred. No. 7.9e-21;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 TKHFTLKSDVLFNFKATLKPEGQALDQ 238
 Db 119 TKHFTLKSDVLFNFKATLKPEGQALDQ 147

RESULT 6
 Q99115 PRELIMINARY; PRT; 244 AA.
 ID Q99115;
 AC Q99115;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Outer membrane protein A (Outer membrane protein II) (Fragment).
 GN OMPA.

OS Escherichia vulneris.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 33821, AND ATCC 33822;
 RX MEDLINE-92065252; PubMed-1955870;
 RA Lawrence J.G., Ochman H., Hartl D.L.;
 RT "Molecular and evolutionary relationships among enteric bacteria.";
 RL J. Gen. Microbiol. 137:1911-1921(1991).
 CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE.
 DR EMBL: M63349; AAA24237.1; -;
 DR HSSP: P02934; IQJP.
 DR InterPro: IPR001145; Bac_OmpA.
 DR InterPro: IPR000498; OmpA_tmern.
 DR Pfam: PF00691; OmpA; 1.
 DR Pfam: PF01389; OmpA_membrane; 1.
 DR PRINTS: PR01021; OMPADOMAIN.
 DR ProDom: PD000930; Bac_OmpA; 1.
 DR PROSITE: PS01068; OmpA; 1.
 KW Outer membrane; Porin; Phage recognition.

FT NON_TER 1 244
 FT NON_TER 244 244
 SQ SEQUENCE 244 AA; 26237 MW; C4D18EB27656EDBA CRC64;

Query Match 8.4%; Score 29; DB 2; Length 244;
 Best Local Similarity 100.0%; Pred. No. 7.9e-21;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 TKHFTLKSDVLFNFKATLKPEGQALDQ 238
 Db 119 TKHFTLKSDVLFNFKATLKPEGQALDQ 147

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RESULT 7
Q93QR2 ID Q93QR2 PRELIMINARY; PRT; 148 AA.
AC Q93QR2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMPA.
OS Erwinia psidii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=69224;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP8427;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF220780; AAK68946.1; -.
DR InterPro: IPR001145; Bac_OmpA.
DR InterPro: IPR000498; OmpA_tmem.
DR Pfam: PF00691; OmpA; 1.
DR Pfam: PF01389; OmpA_membrane; 1.
DR ProDom: PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 148
SQ SEQUENCE 148 AA; 16410 MW; 2BBD1FAC6530167F CRC64;

Query Match
Best Local Similarity 8.1%; Score 28; DB 2; Length 148;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SDVLFNFNKATLKPEGQALDQLYTOLS 244
DB 111 SDVLFNFNKATLKPEGQALDQLYTOLS 138

RESULT 8
Q93QR1 ID Q93QR1 PRELIMINARY; PRT; 148 AA.
AC Q93QR1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMPA.
OS Erwinia psidii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=69224;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP49406;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF220781; AAK68947.1; -.
DR InterPro: IPR001145; Bac_OmpA.
DR InterPro: IPR000498; OmpA_tmem.
DR Pfam: PF00691; OmpA; 1.
DR Pfam: PF01389; OmpA_membrane; 1.
DR ProDom: PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 148
SQ SEQUENCE 148 AA; 16040 MW; 73DDA11D6DFAB00 CRC64;

Query Match
Best Local Similarity 8.1%; Score 28; DB 2; Length 148;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SDVLFNFNKATLKPEGQALDQLYTOLS 244
DB 111 SDVLFNFNKATLKPEGQALDQLYTOLS 138

RESULT 9
Q93QR0 ID Q93QR0 PRELIMINARY; PRT; 148 AA.
AC Q93QR0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMPA.
OS Erwinia psidii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=69224;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP3558;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF220782; AAK68948.1; -.
DR InterPro: IPR001145; Bac_OmpA.
DR InterPro: IPR000498; OmpA_tmem.
DR Pfam: PF00691; OmpA; 1.
DR Pfam: PF01389; OmpA_membrane; 1.
DR ProDom: PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 148
SQ SEQUENCE 148 AA; 16410 MW; 2BBD1FAC6530167F CRC64;

Query Match
Best Local Similarity 8.1%; Score 28; DB 2; Length 148;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SDVLFNFNKATLKPEGQALDQLYTOLS 244
DB 111 SDVLFNFNKATLKPEGQALDQLYTOLS 138

RESULT 10
Q93QP0 ID Q93QP0 PRELIMINARY; PRT; 148 AA.
AC Q93QP0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMPA.
OS Pectobacterium cyripedii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=55209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=29267;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF220802; AAK68968.1; -.
DR InterPro: IPR001145; Bac_OmpA.
DR InterPro: IPR000498; OmpA_tmem.
DR Pfam: PF00691; OmpA; 1.
DR Pfam: PF01389; OmpA_membrane; 1.

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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SDVLFNFNKATLKPEGQALDQLYTOLS 244
DB 111 SDVLFNFNKATLKPEGQALDQLYTOLS 138

RESULT 9
Q93QR0 ID Q93QR0 PRELIMINARY; PRT; 148 AA.
AC Q93QR0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMPA.
OS Erwinia psidii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=69224;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP3558;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF220782; AAK68948.1; -.
DR InterPro: IPR001145; Bac_OmpA.
DR InterPro: IPR000498; OmpA_tmem.
DR Pfam: PF00691; OmpA; 1.
DR Pfam: PF01389; OmpA_membrane; 1.
DR ProDom: PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 148
SQ SEQUENCE 148 AA; 16410 MW; 2BBD1FAC6530167F CRC64;

Query Match
Best Local Similarity 8.1%; Score 28; DB 2; Length 148;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SDVLFNFNKATLKPEGQALDQLYTOLS 244
DB 111 SDVLFNFNKATLKPEGQALDQLYTOLS 138

RESULT 10
Q93QP0 ID Q93QP0 PRELIMINARY; PRT; 148 AA.
AC Q93QP0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Major outer membrane protein (Fragment).
GN OMPA.
OS Pectobacterium cyripedii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=55209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=29267;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF220802; AAK68968.1; -.
DR InterPro: IPR001145; Bac_OmpA.
DR InterPro: IPR000498; OmpA_tmem.
DR Pfam: PF00691; OmpA; 1.
DR Pfam: PF01389; OmpA_membrane; 1.

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DR ProDom; PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 148
SQ SEQUENCE 148 AA; 16013 MW; 17B9503819ADA12F CRC64;

Query Match
Best Local Similarity 8.1%; Score 28; DB 2; Length 148;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 DVLNFNFKATLKPEGQALDQLYTQLS 245
DB 112 DVLNFNFKATLKPEGQALDQLYTQLS 139

RESULT 11
Q93QR4
ID Q93QR4 PRELIMINARY; PRT; 149 AA.
AC Q93QR4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Major outer membrane protein (fragment).
GN OMPA.
OS Erwinia psidii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=69224;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP8428;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220778; AAK68944.1; -.
DR InterPro; IPR001145; Bac_OmpA.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR ProDom; PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 149
SQ SEQUENCE 149 AA; 16380 MW; 5472FFA455195DD5 CRC64;

Query Match
Best Local Similarity 8.1%; Score 28; DB 2; Length 149;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SDVLFNFKATLKPEGQALDQLYTQLS 244
DB 112 SDVLFNFKATLKPEGQALDQLYTQLS 139

RESULT 12
Q93QR3
ID Q93QR3 PRELIMINARY; PRT; 149 AA.
AC Q93QR3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Major outer membrane protein (fragment).
GN OMPA.
OS Erwinia psidii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=69224;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP8428;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
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RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220779; AAK68945.1; -.
DR InterPro; IPR001145; Bac_OmpA.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR ProDom; PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 149
SQ SEQUENCE 149 AA; 16346 MW; 4422BFA4550341D5 CRC64;

Query Match
Best Local Similarity 8.1%; Score 28; DB 2; Length 149;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SDVLFNFKATLKPEGQALDQLYTQLS 244
DB 112 SDVLFNFKATLKPEGQALDQLYTQLS 139

RESULT 13
Q93QP2
ID Q93QP2 PRELIMINARY; PRT; 149 AA.
AC Q93QP2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Major outer membrane protein (fragment).
GN OMPA.
OS Erwinia rhapontici.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=55212;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=29283;
RA Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT "Allelic diversity of the major outer membrane protein (ompA) gene
RT among necrogenic phytopathogenic species: Molecular evolutionary
RT aspects of relatedness.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220800; AAK68966.1; -.
DR InterPro; IPR001145; Bac_OmpA.
DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR ProDom; PD000930; Bac_OmpA; 1.
FT NON_TER 1
FT NON_TER 149
SQ SEQUENCE 149 AA; 16004 MW; 8E0642C39DFAF216 CRC64;

Query Match
Best Local Similarity 7.6%; Score 26; DB 2; Length 149;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 LFNFNKATLKPEGQALDQLYTQLS 245
DB 115 LFNFNKATLKPEGQALDQLYTQLS 140

RESULT 14
Q93QO6
ID Q93QO6 PRELIMINARY; PRT; 147 AA.
AC Q93QO6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Major outer membrane protein (fragment).
GN OMPA.
OS Brenneria rubrifaciens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Brenneria.
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OX  NCBI_TaxID=55213;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BR4790;
RA  Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT  "Allelic diversity of the major outer membrane protein (ompA) gene
RT  among necrogenic phytopathogenic species: Molecular evolutionary
RT  aspects of relatedness.";
RL  Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF220786; AAK68952.1; -;
DR  InterPro; IPR001145; Bac_OmpA.
DR  InterPro; IPR000498; OmpA_tmem.
DR  Pfam; PF00691; OmpA; 1.
DR  Pfam; PF01389; OmpA_membrane; 1.
FT  NON_TER 1
FT  NON_TER 147 149
SQ  SEQUENCE 147 AA; 16020 MW; 92F431FC41442DC4 CRC64;

Query Match
Best Local Similarity 6.4%; Score 22; DB 2; Length 147;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 213 FTLKSDVLFNFENKATLKPEGOQ 234
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Db 106 FTLKSDVLFNFENKATLKPEGOQ 127

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RESULT 15
Q93QP5
ID  Q93QP5 PRELIMINARY; PRT; 149 AA.
AC  Q93QP5;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Major outer membrane protein (Fragment).
GN  OMPA.
OS  Erwinia mallotivora.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC  Erwiniinae.
OX  NCBI_TaxID=69222;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=EM8645;
RA  Brown E.W., Davis R.M., Gouk C., van der Zwet T.;
RT  "Allelic diversity of the major outer membrane protein (ompA) gene
RT  among necrogenic phytopathogenic species: Molecular evolutionary
RT  aspects of relatedness.";
RL  Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF220797; AAK68963.1; -;
DR  InterPro; IPR001145; Bac_OmpA.
DR  InterPro; IPR000498; OmpA_tmem.
DR  Pfam; PF00691; OmpA; 1.
DR  Pfam; PF01389; OmpA_membrane; 1.
DR  ProDom; PD000930; Bac_OmpA; 1.
FT  NON_TER 1
FT  NON_TER 149 149
SQ  SEQUENCE 149 AA; 16100 MW; 3494978343ED9A6C CRC64;

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Query Match
Best Local Similarity 6.4%; Score 22; DB 2; Length 149;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 223 FNKATLKPEGGQALDQLYTQLS 244
    |||||
Db 118 FNKATLKPEGGQALDQLYTQLS 139

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Search completed: April 15, 2003, 08:56:27
Job time : 71 secs